GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:04 ; Search time 20.73 Seconds
(without alignments)
144.928 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	2	US-08-561-521-11	Sequence 11, Appl
2	655	100.0	123	5	PCT-US95-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appli
6	552	84.3	123	5	PCT-US95-01219-9	Sequence 9, Appli
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appli
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appli
9	523.5	79.9	120	4	US-08-871-488A-19	Sequence 19, Appl
10	523	79.8	117	4	US-08-646-265A-132	Sequence 132, App
11	523	79.8	136	4	US-08-646-265A-99	Sequence 99, Appl
12	523	79.8	269	4	US-08-646-265A-109	Sequence 109, App
13	515	78.6	119	2	US-08-561-521-13	Sequence 13, Appl
14	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
15	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
16	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
17	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
18	505	77.1	125	5	PCT-US95-01219-44	Sequence 44, Appl
19	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
20	495	75.6	119	5	PCT-US95-01219-10	Sequence 10, Appl
21	492	75.1	117	2	US-08-290-592E-17	Sequence 17, Appl
22	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
23	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
24	491.5	75.0	118	2	US-08-232-081B-8	Sequence 8, Appli
25	489.5	74.7	120	4	US-09-025-769B-36	Sequence 36, Appl
26	489.5	74.7	120	4	US-09-025-769B-59	Sequence 59, Appl
27	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
28	484.5	74.0	135	1	US-08-137-117D-112	Sequence 112, App
29	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
30	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
31	484.5	74.0	139	2	US-08-452-164A-19	Sequence 19, Appl
32	484.5	74.0	139	3	US-08-603-024-18	Sequence 18, Appl
33	481	73.4	121	1	US-08-202-047-23	Sequence 23, Appl
34	481	73.4	121	3	US-08-964-690-23	Sequence 23, Appl
35	474	72.4	140	3	US-08-836-561-74	Sequence 74, Appl
36	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
37	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
38	473	72.2	123	2	US-08-487-113D-53	Sequence 53, Appl
39	473	72.2	123	2	US-08-473-503-53	Sequence 53, Appl
40	473	72.2	123	2	US-08-483-932-53	Sequence 53, Appl
41	473	72.2	123	2	US-08-720-420A-53	Sequence 53, Appl
42	473	72.2	123	3	US-08-714-017-53	Sequence 53, Appl
43	473	72.2	123	3	US-08-475-680-53	Sequence 53, Appl
44	472	72.1	123	1	US-08-482-882-86	Sequence 86, Appl
45	472	72.1	123	2	US-08-483-389-86	Sequence 86, Appl

ALIGNMENTS

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RESULT 1
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-11

  Query Match           100.0%;  Score 655;  DB 2;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-58;
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  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123


RESULT   2
PCT-US95-01219-11
; Sequence 11, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-11


  Query Match           100.0%;  Score 655;  DB 5;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-58;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy     121 VSS 123
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Db     121 VSS 123


RESULT   3
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-17


  Query Match           100.0%;  Score 655;  DB 2;  Length 142;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-58;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db      20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy     121 VSS 123
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Db     140 VSS 142


RESULT   4
PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
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; GENERAL INFORMATION:
;   APPLICANT:  Bendig, Mary M.
;   APPLICANT:  Leger, Olivier J.
;   APPLICANT:  Saldanha, Jose
;   APPLICANT:  Jones, S. Tarran
;   TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION:  Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES:  45
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend Khourie and Crew
;     STREET:  One Market Plaza, Steuart Tower, Suite 2000
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US95/01219
;     FILING DATE:  25-JAN-1995
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/186,269
;     FILING DATE:  25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Smith, William L.
;     REGISTRATION NUMBER:  30,223
;     REFERENCE/DOCKET NUMBER:  15270-14
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-543-9600
;     TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  142 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
PCT-US95-01219-17

  Query Match             100.0%;  Score 655;  DB 5;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-58;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy     121 VSS 123
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Db     140 VSS 142


RESULT   5
US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;     APPLICANT:  Bendig, Mary M.
;     APPLICANT:  Leger, Olivier J.
;     APPLICANT:  Saldanha, Jose
;     APPLICANT:  Jones, S. Tarran
;     TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;     TITLE OF INVENTION:  Adhesion Molecule VLA-4
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/561,521
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,269A
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  123 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-561-521-9

  Query Match             84.3%;  Score 552;  DB 2;  Length 123;
  Best Local Similarity   82.9%;  Pred. No. 3.5e-48;
  Matches  102;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :||| ||||| |||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||: |||||||::|||::|||| ||||||:|||||||||||||||||||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy     121 VSS 123
          |||
Db     121 VSS 123


RESULT   6
PCT-US95-01219-9
; Sequence 9, Application PC/TUS9501219
;  GENERAL INFORMATION:
;     APPLICANT:  Bendig, Mary M.
;     APPLICANT:  Leger, Olivier J.
;     APPLICANT:  Saldanha, Jose
;     APPLICANT:  Jones, S. Tarran
;     TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;     TITLE OF INVENTION:  Adhesion Molecule VLA-4
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-9

Query Match 84.3%; Score 552; DB 5; Length 123;
Best Local Similarity 82.9%; Pred. No. 3.5e-48;
Matches 102; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| : ||||||| :|| |||||||||||| |:| | | |||:|||||||||||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| : ||||||| : :|||::|||| ||||||| :|||||||||||||||||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123
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RESULT 7
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-4

Query Match 83.1%; Score 544; DB 2; Length 140;
Best Local Similarity 82.6%; Pred. No. 2.6e-47;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| : ||||||| :|| |||||||||||| |:| | | |||:|||||||||||
Db      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| : ||||||| : :|||::|||| ||||||| :|||||||||||||||||||||| ||
Db      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy     121 V 121
           |
Db     140 V 140
```

RESULT 8
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-4


  Query Match             83.1%;  Score 544;  DB 5;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 2.6e-47;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||| |:| | | |||:|||||||||||
Db      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||: ||||||::|||::|||| |||||||:||||||||||||||||||||| ||
Db      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy     121 V 121
           |
Db     140 V 140


RESULT   9
US-08-871-488A-19
; Sequence 19, Application US/08871488A
; Patent No. 6358710
;  GENERAL INFORMATION:
;    APPLICANT:  Graves, Scott S.
;    APPLICANT:  Reno, John M.
;    APPLICANT:  Mallett, Robert W.
;    APPLICANT:  Hylarides, Mark D.
;    APPLICANT:  Searle, Stephen M.J.
;    APPLICANT:  Henry, Andrew H.
;    APPLICANT:  Pedersen, Jan T.
;    APPLICANT:  Rees, Anthony R.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES THAT BIND TO THE
;    TITLE OF INVENTION:  ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
;    TITLE OF INVENTION:  PRETARGETING METHODS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/871,488A
;      FILING DATE:  09-JUN-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey Ph.D., Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  690022.527C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-871-488A-19


  Query Match             79.9%;  Score 523.5;  DB 4;  Length 120;
  Best Local Similarity   82.9%;  Pred. No. 2.4e-45;
  Matches  102;  Conservative    8;  Mismatches   10;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||||||:||||||||| |:|||||||||| ||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKC 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           | |||||||||||| :|||||||||||:||||||:||      | :::|||||||||||
Db      61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117

Qy     121 VSS 123
           |||
Db     118 VSS 120


RESULT  10
US-08-646-265A-132
; Sequence 132, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-132


  Query Match             79.8%;  Score 523;  DB 4;  Length 117;
  Best Local Similarity   83.7%;  Pred. No. 2.6e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||||| ||||||||||:| |||
```

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Db      1 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db     61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114

Qy    121 VSS 123
          |||
Db    115 VSS 117


RESULT  11
US-08-646-265A-99
; Sequence 99, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  136 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-99


  Query Match           79.8%;  Score 523;  DB 4;  Length 136;
  Best Local Similarity  83.7%;  Pred. No. 3.1e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||:|||||||||||||||||||||||||||| ||||||||||:| |||
Db     20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db     80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133

Qy    121 VSS 123
          |||
Db    134 VSS 136


RESULT  12
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  269 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-109


  Query Match           79.8%;  Score 523;  DB 4;  Length 269;
  Best Local Similarity  83.7%;  Pred. No. 6.9e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||:|||||||||||||||||||||||||||| ||||||||||:| |||
Db     23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db     83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 136

Qy    121 VSS 123
          |||
Db    137 VSS 139


RESULT  13
```

```
US-08-561-521-13
; Sequence 13, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-13


  Query Match           78.6%;  Score 515;  DB 2;  Length 119;
  Best Local Similarity  82.9%;  Pred. No. 1.7e-44;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||   :|||||||||||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||||||||||||||||||||||||| ||:|:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  14
PCT-US95-01219-13
; Sequence 13, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-13


  Query Match           78.6%;  Score 515;  DB 5;  Length 119;
  Best Local Similarity  82.9%;  Pred. No. 1.7e-44;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||   :|||||||||||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||||||||||||||||||||||||| ||:|:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  15
US-08-561-521-12
; Sequence 12, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
```

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;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/561,521
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,269A
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-561-521-12


  Query Match           78.2%;  Score 512;  DB 2;  Length 119;
  Best Local Similarity  82.9%;  Pred. No. 3.3e-44;
  Matches  102;  Conservative    4;  Mismatches   13;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||||   :|||||||| |||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             |||||||||||||||||||||||||||||||||| |||:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYYGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


Search completed: July  9, 2002, 15:39:04
Job time: 30 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 ; Search time 28.27 Seconds
(without alignments)
360.293 Million cell updates/sec

Title: US-09-010-377-1
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488	86.8	104	2	S26330	Ig kappa chain V r
2	479	85.2	104	2	S26329	Ig kappa chain V r
3	478	85.1	106	2	C33936	Ig kappa chain V r
4	463.5	82.5	125	2	S09365	Ig kappa chain - m
5	452	80.4	97	2	PH1064	Ig light chain V r
6	446.5	79.4	107	2	PL0270	Ig kappa chain V r
7	443.5	78.9	108	1	K1HURE	Ig kappa chain V-I
8	443.5	78.9	129	2	S52789	Ig kappa chain V r
9	443	78.8	103	2	S26332	Ig light chain V r
10	440.5	78.4	107	2	PL0272	Ig kappa chain V r
11	440	78.3	94	2	E33730	Ig kappa chain V r
12	439.5	78.2	107	2	PL0269	Ig kappa chain V r
13	439.5	78.2	107	2	PL0271	Ig kappa chain V r
14	439.5	78.2	108	1	K1HUAU	Ig kappa chain V-I
15	435.5	77.5	108	2	I39154	Ig kappa chain (BR
16	429.5	76.4	110	2	S44118	Ig kappa chain V-J
17	429.5	76.4	127	2	S40367	Ig kappa chain V-J
18	426	75.8	107	2	S36275	Ig lambda chain V
19	424.5	75.5	125	2	S40333	Ig kappa chain V-J
20	421.5	75.0	108	1	K1HULY	Ig kappa chain V-I
21	419.5	74.6	108	1	K1HUAG	Ig kappa chain V-I
22	419.5	74.6	108	1	K1HURY	Ig kappa chain V-I
23	418.5	74.5	123	2	S40331	Ig kappa chain - h
24	415.5	73.9	109	2	S31998	Ig kappa chain - h
25	414.5	73.8	131	2	S40352	Ig kappa chain V-J
26	414	73.7	124	2	S40336	Ig kappa chain V-J
27	413.5	73.6	108	1	K1HUSW	Ig kappa chain V-I
28	412.5	73.4	108	2	B49047	Ig kappa chain V r
29	412	73.3	106	2	PC2397	anti-tetanus toxin
30	410.5	73.0	108	2	S44122	Ig kappa chain V r
31	410.5	73.0	109	2	S31981	Ig kappa chain - h
32	409.5	72.9	129	1	K1HUWK	Ig kappa chain pre
33	409	72.8	107	1	K1HUAR	Ig kappa chain V-I
34	408.5	72.7	108	1	K1HUWE	Ig kappa chain V-I
35	408.5	72.7	139	2	S40365	Ig kappa chain - h
36	407.5	72.5	141	2	A49134	Ig kappa chain V-I
37	405.5	72.2	117	2	S46371	Ig kappa chain V-J
38	405	72.1	108	2	S30521	Ig kappa chain V r
39	404.5	72.0	132	2	S40334	Ig kappa chain - h
40	403.5	71.8	94	2	PH1063	Ig light chain V r
41	403.5	71.8	107	2	S36264	Ig lambda chain V
42	403.5	71.8	127	2	S11240	Ig kappa chain V r
43	403	71.7	117	2	S43528	Ig kappa chain V r
44	403	71.7	117	2	S42263	Ig kappa chain V r
45	402.5	71.6	108	1	K1HUHU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 488; DB 2; Length 104;
Best Local Similarity 85.6%; Pred. No. 1.6e-35;
Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||:| :|||||| |||||||:|||| ||| ||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
          ||||||||||:|:||:|:|||||||||||||||||||| |||:|
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104
```

RESULT 2
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
  Query Match             85.2%;  Score 479;  DB 2;  Length 104;
  Best Local Similarity   84.6%;  Pred. No. 9.7e-35;
  Matches   88;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
           ||||||||||:|:|:|:|||||||||||||||:||| |||:|
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104


RESULT   3
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             85.1%;  Score 478;  DB 2;  Length 106;
  Best Local Similarity   83.0%;  Pred. No. 1.2e-34;
  Matches   88;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:|:|:| ||:|||||||||:|:||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106


RESULT   4
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm
A;Reference number: S09365; MUID:90098844
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>


  Query Match             82.5%;  Score 463.5;  DB 2;  Length 125;
  Best Local Similarity   83.2%;  Pred. No. 2.5e-33;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db      18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW-TFGQGTKVEIK 106
           |||||||| ||:|:||:| |||||||||||||||  ||| |||:|||
Db      78 RFSGSGSGSDYSFSISNLGPEDIATYYCLQYDNLLRTFGGGTKLEIK 124


RESULT   5
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             80.4%;  Score 452;  DB 2;  Length 97;
  Best Local Similarity   85.6%;  Pred. No. 1.9e-32;
  Matches   83;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
           |||||||||||:|:|:|:|||||||||||||||:||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97


RESULT   6
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             79.4%;  Score 446.5;  DB 2;  Length 107;
  Best Local Similarity   79.4%;  Pred. No. 6.4e-32;
  Matches   85;  Conservative   11;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||| |||||:|:|:|||||:|||||:|  || ||||| ||| ||||||||
Db       1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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                 |||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT   7
K1HURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom k
 vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:76023758
A;Accession: A91663
A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
A;Reference number: A90392; MUID:76039968
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental


  Query Match             78.9%;  Score 443.5;  DB 1;  Length 108;
  Best Local Similarity   81.1%;  Pred. No. 1.2e-31;
  Matches   86;  Conservative    9;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| ||: ||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           |||||||| |||||||||||||||||||| || :| :|||||||::|
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106


RESULT   8
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>


  Query Match             78.9%;  Score 443.5;  DB 2;  Length 129;
  Best Local Similarity   79.4%;  Pred. No. 1.4e-31;
  Matches   85;  Conservative   10;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| ||||:|||  |:|: |:||
Db      23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |::||||||||||:|||| |||||  ||| |||||||
Db      83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129


RESULT   9
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             78.8%;  Score 443;  DB 2;  Length 103;
  Best Local Similarity   77.7%;  Pred. No. 1.2e-31;
  Matches   80;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|| ||| | || :|:|||  ||| |||:: |||:||||||||
Db       1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKV 103
           ||||||||||:|:|||:|:|||||||||||||||:||| |||:
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103


RESULT   10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
```

```
  Query Match           78.4%;  Score 440.5;  DB 2;  Length 107;
  Best Local Similarity  78.5%;  Pred. No. 2.1e-31;
  Matches   84;  Conservative   11;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||| |||||:||:| |||:||||||:| |||||   || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  11
E33730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325
A;Accession: E33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match           78.3%;  Score 440;  DB 2;  Length 94;
  Best Local Similarity  86.2%;  Pred. No. 2e-31;
  Matches   81;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
           ||||||||||:|:||:|:|||||||||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94


RESULT  12
PL0269
Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match           78.2%;  Score 439.5;  DB 2;  Length 107;
  Best Local Similarity  78.5%;  Pred. No. 2.6e-31;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:||:| | |:||||| | |||||   || ||||| ||| |||||||
Db       1 DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  13
PL0271
Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match           78.2%;  Score 439.5;  DB 2;  Length 107;
  Best Local Similarity  78.5%;  Pred. No. 2.6e-31;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||| |||||:||:| |||:||||| | |||||   || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  14
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ,
A;Reference number: A91653; MUID:72189444
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones prote
A;Reference number: A90729; MUID:77022433
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances
```

```
A;Reference number: S02572; MUID:88005152
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted


  Query Match             78.2%;  Score 439.5;  DB 1;  Length 108;
  Best Local Similarity   79.4%;  Pred. No. 2.6e-31;
  Matches   85;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| ||||| |||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| |||  :|||||||||||||||| ||| | ||||||||||||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107


RESULT  15
I39154
Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A;Reference number: I39154; MUID:96003804
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             77.5%;  Score 435.5;  DB 2;  Length 108;
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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| |||| |||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| :|||||||||||||||||| |||:| :|||||||||||
Db      61 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIK 107


Search completed: July  9, 2002, 15:39:38
Job time: 64 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:44 ; Search time 15.81 Seconds
(without alignments)
259.600 Million cell updates/sec

Title: US-09-010-377-1
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	443.5	78.9	108	1	KV1O_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1	KV1B_HUMAN	P01594 homo sapien
3	421.5	75.0	108	1	KV1M_HUMAN	P01605 homo sapien
4	419.5	74.6	108	1	KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1	KV1P_HUMAN	P01608 homo sapien
6	419.5	74.6	108	1	KV1Y_HUMAN	P80362 homo sapien
7	413.5	73.6	108	1	KV1Q_HUMAN	P01609 homo sapien
8	409.5	72.9	129	1	KV1W_HUMAN	P04431 homo sapien
9	409	72.8	107	1	KV1D_HUMAN	P01596 homo sapien
10	408.5	72.7	108	1	KV1R_HUMAN	P01610 homo sapien
11	402.5	71.6	108	1	KV1H_HUMAN	P01600 homo sapien
12	397.5	70.7	108	1	KV1F_HUMAN	P01598 homo sapien
13	396.5	70.6	108	1	KV1V_HUMAN	P04430 homo sapien
14	390.5	69.5	108	1	KV1K_HUMAN	P01603 homo sapien
15	388.5	69.1	108	1	KV1E_HUMAN	P01597 homo sapien
16	386.5	68.8	108	1	KV1L_HUMAN	P01604 homo sapien
17	385.5	68.6	108	1	KV1N_HUMAN	P01606 homo sapien
18	384.5	68.4	108	1	KV1C_HUMAN	P01595 homo sapien
19	383.5	68.2	108	1	KV1G_HUMAN	P01599 homo sapien
20	383.5	68.2	129	1	KV1X_HUMAN	P04432 homo sapien
21	381.5	67.9	108	1	KV1S_HUMAN	P01611 homo sapien
22	376.5	67.0	134	1	KV4C_HUMAN	P06314 homo sapien
23	371.5	66.1	108	1	KV5J_MOUSE	P01643 mus musculu
24	368	65.5	117	1	KV1J_HUMAN	P01602 homo sapien
25	366.5	65.2	128	1	KV5E_MOUSE	P01637 mus musculu
26	365	64.9	133	1	KV4B_HUMAN	P06313 homo sapien
27	364.5	64.9	108	1	KV5O_MOUSE	P01648 mus musculu
28	363.5	64.7	108	1	KV5N_MOUSE	P01647 mus musculu
29	362	64.4	109	1	KV1T_HUMAN	P01612 homo sapien
30	362	64.4	117	1	KV1I_HUMAN	P01601 homo sapien
31	361.5	64.3	108	1	KV5K_MOUSE	P01644 mus musculu
32	359.5	64.0	108	1	KV5M_MOUSE	P01646 mus musculu
33	358.5	63.8	108	1	KV5L_MOUSE	P01645 mus musculu
34	356.5	63.4	112	1	KV1U_HUMAN	P01613 homo sapien
35	348.5	62.0	114	1	KV4A_HUMAN	P01625 homo sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207 homo sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653 mus musculu
39	345	61.4	115	1	KV5F_MOUSE	P01638 mus musculu
40	341.5	60.8	108	1	KV5Q_MOUSE	P01650 mus musculu
41	341	60.7	109	1	KV3E_HUMAN	P01623 homo sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652 mus musculu
43	339.5	60.4	108	1	KV5U_MOUSE	P04946 mus musculu
44	339	60.3	109	1	KV3D_HUMAN	P01622 homo sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624 homo sapien

ALIGNMENTS

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RESULT  1
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ID   KV1O_HUMAN     STANDARD;      PRT:   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; K1HURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
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FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;


  Query Match             78.9%;  Score 443.5;  DB 1;  Length 108;
  Best Local Similarity   81.1%;  Pred. No. 5.9e-40;
  Matches   86;  Conservative    9;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| ||: ||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           |||||||| |||||||||||||||||||| || :| :|||||||::|
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106


RESULT   2
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; K1HUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;


  Query Match             78.2%;  Score 439.5;  DB 1;  Length 108;
  Best Local Similarity   79.4%;  Pred. No. 1.5e-39;
  Matches   85;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| |||||:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| |||  :|||||||||||||||||| ||| | ||||||||||||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107


RESULT   3
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;


  Query Match             75.0%;  Score 421.5;  DB 1;  Length 108;
  Best Local Similarity   75.0%;  Pred. No. 1.2e-37;
  Matches   81;  Conservative   11;  Mismatches   13;  Indels    3;  Gaps    2;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||| |||||||||: ||::| |: |||| || ||:|||:  |  : |:||
Db       1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
           |||||||||||||||||||||||||||||||||||  |||||||||||
Db      61 RFSGSGSGTDFTLTISSLQPEDIATYYCQQYDNLWTWTFGQGTKVEIK 108
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Db     61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK 107


RESULT   4
KV1A_HUMAN
ID   KV1A_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   76.6%;  Pred. No. 2e-37;
  Matches   82;  Conservative    9;  Mismatches   15;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||: ||||| |: |||| | |||::||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKLLIYDASNLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||| | |:|||| |||||||||| ||| |  ||||||:|||
Db      61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107


RESULT   5
KV1P_HUMAN
ID   KV1P_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; K1HURY.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   75.7%;  Pred. No. 2e-37;
  Matches   81;  Conservative   12;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||: ||||: :: |||| |||||:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||:||| |:|||||||||||||||| |:|||  ||| |||| |
Db      61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107


RESULT   6
KV1Y_HUMAN
ID   KV1Y_HUMAN      STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
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RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   75.7%;  Pred. No. 2e-37;
  Matches   81;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||: |||| |:: ||: ||::||:|:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| (:|||||||||||||||||| ||| |  ||| ||||:||
Db      61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107


RESULT   7
KV1Q_HUMAN
ID   KV1Q_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01609;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Scw.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059271; PubMed=4435756;
RA   Eulitz M., Hilschmann N.;
RT   "The primary structure of a human immunoglobulin L-chain of
RT   kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides
RT   and the complete amino acid sequence.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01875; K1HUSW.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11764 MW;  32CECDDDF9644414 CRC64;


  Query Match             73.6%;  Score 413.5;  DB 1;  Length 108;
  Best Local Similarity   74.8%;  Pred. No. 8.4e-37;
  Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||: |||| |:: || | |||||||||: | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIRKHLNWYDQKPGKAPRLLIYGASTLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |:| |||:|||||  ||| ||||:  ||||||:|| |
Db      61 RFSGSGSGTDFTLTISTLQPEDIGNYYCQQYDNVPITFGQGTRVENK 107


RESULT   8
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;


  Query Match             72.9%;  Score 409.5;  DB 1;  Length 129;
  Best Local Similarity   74.8%;  Pred. No. 2.7e-36;
  Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |: |||| |||||:|||:  |:|| |: |
Db      23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82
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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           ||||||||| |:| |||||||||| ||||| | |  | |||||||:|||
Db      83 RFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQGTRLEIK 129


RESULT  9
KV1D_HUMAN
ID   KV1D_HUMAN      STANDARD;       PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; K1HUAR.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .).
FT   NON_TER      107    107
SQ   SEQUENCE   107 AA;  11703 MW;  E1BF0DF9844C3346 CRC64;


  Query Match             72.8%;  Score 409;  DB 1;  Length 107;
  Best Local Similarity   68.9%;  Pred. No. 2.5e-36;
  Matches   73;  Conservative   20;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||:|||||||||| |||: ||:|: ::|||| |||||::||: :|:|: |:||
Db       1 DIQMTQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||| |:| |||||:|:: ||||| ||:  :||| ||||:||
Db      61 RFSGSGSGTDFTLTISSLZPBBFATYYCQQYNTFFTFGPGTKVDIK 106


RESULT  10
KV1R_HUMAN
ID   KV1R_HUMAN      STANDARD;       PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Franglone B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; K1HUWE.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Monoclonal antibody.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN       24    34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35    49       FRAMEWORK-2.
FT   DOMAIN       50    56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57    88       FRAMEWORK-3.
FT   DOMAIN       89    97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23    88       BY SIMILARITY.
FT   NON_TER      108   108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;


  Query Match             72.7%;  Score 408.5;  DB 1;  Length 108;
  Best Local Similarity   72.0%;  Pred. No. 2.8e-36;
  Matches   77;  Conservative   12;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |   : |||| || ||: ||:  ::|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| ::| ||:|||||| ||||||||  :  ||||||||||:|
Db      61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107


RESULT  11
KV1H_HUMAN
ID   KV1H_HUMAN      STANDARD;       PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; K1HUHU.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN       24    34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35    49       FRAMEWORK-2.
FT   DOMAIN       50    56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57    88       FRAMEWORK-3.
FT   DOMAIN       89    97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23    88       BY SIMILARITY.
FT   NON_TER      108   108
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SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

  Query Match             71.6%;  Score 402.5;  DB 1;  Length 108;
  Best Local Similarity   72.9%;  Pred. No. 1.2e-35;
  Matches   78;  Conservative   12;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |::|||| |||||::||:  |:|  |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           |||||||| |:| |||||||| ||||| | |    :|||||:|||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIK 107


RESULT  12
KV1F_HUMAN
ID   KV1F_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01866; K1HUEU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11788 MW;  9CD294F2F4D88823 CRC64;

  Query Match             70.7%;  Score 397.5;  DB 1;  Length 108;
  Best Local Similarity   70.1%;  Pred. No. 4e-35;
  Matches   75;  Conservative   16;  Mismatches   15;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||:|||||||||||||: || || ::||||| |||||:||::  |:|: |:||
Db       1 DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
           || ||||| ::| ||||||||:| ||||| ||: :   ||||||||:|
Db      61 RFIGSGSGTEFTLTISSLQPDDFATYYCQQYNSDSKMFGQGTKVEVK 107


RESULT  13
KV1V_HUMAN
ID   KV1V_HUMAN     STANDARD;      PRT;   108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region BAN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
DR   PIR; A01878; K1HUBN.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  CD3FD944FE96FD37 CRC64;

  Query Match             70.6%;  Score 396.5;  DB 1;  Length 108;
  Best Local Similarity   70.1%;  Pred. No. 5.1e-35;
  Matches   75;  Conservative   14;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:|||||||||||||||||||: || :  |:|||:|| |||||: ||:  | || |:||
Db       1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |:|||||  |:  |||||||||| ||||| ||::  :|||||||:|||
Db      61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107


RESULT  14
KV1K_HUMAN
ID   KV1K_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
```

```
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; K1HUKA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN      24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49       FRAMEWORK-2.
FT   DOMAIN      50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88       FRAMEWORK-3.
FT   DOMAIN      89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107       FRAMEWORK-4.
FT   DISULFID    23     88       BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;


  Query Match             69.5%;  Score 390.5;  DB 1;  Length 108;
  Best Local Similarity   66.4%;  Pred. No. 2.2e-34;
  Matches   71;  Conservative   19;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||:|| |||||||||||: || :  |: |||| |||||:|||:  |:|: |:||
Db       1 DIQMTQSPSTLSVSVGDRVTITCEASQTVLSYLNWYQQKPGKAPKLLIYAASSLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| ||| ::|||||||::|:: ||||| :| :|  ||||||||::|
Db      61 RFSGQGSGTBFTFTISSVZPZBFATYYCQZYLDLPRTFGQGTKVDLK 107


RESULT  15
KV1E_HUMAN
ID   KV1E_HUMAN      STANDARD;       PRT;   108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01865; K1HUDE.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN      24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49       FRAMEWORK-2.
FT   DOMAIN      50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88       FRAMEWORK-3.
FT   DOMAIN      89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107       FRAMEWORK-4.
FT   DISULFID    23     88       BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11661 MW;  BDD6E350017F1E51 CRC64;


  Query Match             69.1%;  Score 388.5;  DB 1;  Length 108;
  Best Local Similarity   68.9%;  Pred. No. 3.6e-34;
  Matches   73;  Conservative   13;  Mismatches   19;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           :|:|||||||||||||||||||||:  | :|||: |||| |||||::||   |:|: |:||
Db       1 BIZMTQSPSSLSASVGDRVTITCRAGQSVNKYLNWYQQKPGKAPKVLIFAASSLKSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEI 105
           |||||||| |:| ||| | ||| ||||| | |   :||| |||||:
Db      61 RFSGSGSGTDFTLTISGLLPEDFATYYCQQSYTTPYTFGPGTKVEM 106


Search completed: July  9, 2002, 15:45:57
Job time: 373 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:09 ; Search time 43.02 Seconds
(without alignments)
426.254 Million cell updates/sec

Title: US-09-010-377-1
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77	Q9ul77 homo sapien
2	418	74.4	241	11	Q921A6	Q921a6 mus musculu
3	414	73.7	107	4	Q96SA9	Q96sa9 homo sapien
4	406.5	72.3	108	4	Q9UL70	Q9ul70 homo sapien
5	395	70.3	107	4	Q9UL81	Q9ul81 homo sapien
6	385.5	68.6	108	4	Q9UL79	Q9ul79 homo sapien
7	384.5	68.4	214	11	Q9R1A5	Q9r1a5 mus musculu
8	379.5	67.5	233	11	Q91WS9	Q91ws9 mus musculu
9	365.5	65.0	116	4	Q96PF6	Q96pf6 homo sapien
10	362.5	64.5	107	11	Q9JL84	Q9jl84 mus musculu
11	355.5	63.3	234	11	Q91WF8	Q91wf8 mus musculu
12	353.5	62.9	109	11	Q920E6	Q920e6 mus musculu
13	337.5	60.1	298	11	Q9QYF0	Q9qyf0 mus musculu
14	336.5	59.9	108	4	Q9UL83	Q9ul83 homo sapien
15	332	59.1	109	4	Q9UL85	Q9ul85 homo sapien
16	331	58.9	109	4	Q9UL78	Q9ul78 homo sapien
17	329	58.5	109	4	Q9UL86	Q9ul86 homo sapien
18	322.5	57.4	127	11	Q925S9	Q925s9 mus musculu
19	307.5	54.7	107	11	Q9ERZ9	Q9erz9 mus musculu
20	306.5	54.5	111	11	Q920E9	Q920e9 mus musculu
21	303.5	54.0	211	11	Q91XL0	Q91xl0 mus musculu
22	302.5	53.8	99	11	Q9JL74	Q9jl74 mus musculu
23	297	52.8	106	5	Q9U410	Q9u410 schistosoma
24	294	52.3	238	11	Q99M37	Q99m37 mus musculu
25	292.5	52.0	114	4	Q9UL80	Q9ul80 homo sapien
26	284.5	50.6	101	11	Q9JL78	Q9jl78 mus musculu
27	284	50.5	235	11	Q91W12	Q91w12 mus musculu
28	281.5	50.1	97	11	Q9JL76	Q9jl76 mus musculu
29	273.5	48.7	109	6	Q9N0W5	Q9n0w5 oryctolagus
30	269.5	48.0	103	11	Q9JL80	Q9jl80 mus musculu
31	255	45.4	104	11	Q9JL82	Q9jl82 mus musculu
32	212.5	37.8	107	4	Q9UL82	Q9ul82 homo sapien
33	210	37.4	108	4	Q96SB0	Q96sb0 homo sapien
34	206	36.7	107	4	Q9NSD6	Q9nsd6 homo sapien
35	202	35.9	236	4	Q96E61	Q96e61 homo sapien
36	201	35.8	112	4	Q96JD1	Q96jd1 homo sapien
37	190.5	33.9	112	4	Q96JD2	Q96jd2 homo sapien
38	190.5	33.9	116	4	Q96JD0	Q96jd0 homo sapien
39	184	32.7	218	11	Q925S1	Q925s1 mus musculu
40	183	32.6	109	11	Q9ET13	Q9et13 mus musculu
41	179	31.9	233	11	Q91V32	Q91v32 m adult mal
42	170	30.2	130	4	Q9NP29	Q9np29 homo sapien
43	168	29.9	235	11	Q99M11	Q99m11 mus musculu
44	166	29.5	233	4	Q96I69	Q96i69 homo sapien
45	165	29.4	337	13	Q9IB02	Q9ib02 sphoeroides

ALIGNMENTS

RESULT 1
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 76.2%; Score 428.5; DB 4; Length 108;
Best Local Similarity 76.6%; Pred. No. 1.1e-40;
Matches 82; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||: || |: |: |||| ||||| |||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           ||||||||| |:| |||||||||| ||||| | |   ||||:|||||||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107


RESULT   2
Q921A6
ID   Q921A6      PRELIMINARY;      PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
DR   EMBL; U88067; AAB48044.1; -.
FT   NON_TER       1      1
FT   NON_TER     241    241
SQ   SEQUENCE   241 AA;  26086 MW;  0276887248E9C771 CRC64;


  Query Match             74.4%;  Score 418;  DB 11;  Length 241;
  Best Local Similarity   73.6%;  Pred. No. 4.5e-39;
  Matches   78;  Conservative   12;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||::|||||||||||:| :|||||| ||||||||:|||| ||| ||        :||||||
Db     134 DIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSAHTLHIYIQPGIPS 193

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||| |||| ||| |||:|:|
Db     194 RFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLHTFGGGTKLELK 239


RESULT   3
Q96SA9
ID   Q96SA9      PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;


  Query Match             73.7%;  Score 414;  DB 4;  Length 107;
  Best Local Similarity   75.5%;  Pred. No. 4.8e-39;
  Matches   80;  Conservative    9;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |: |||| |||||:|||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||| |:| |||||||||| ||||| |  :  ||| |||||||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIK 106


RESULT   4
Q9UL70
ID   Q9UL70      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;


  Query Match             72.3%;  Score 406.5;  DB 4;  Length 108;
  Best Local Similarity   72.9%;  Pred. No. 3.4e-38;
  Matches   78;  Conservative   12;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||:|||: || |: |:|||| ||| |: ||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |:| ||||||||||:|||| :|::   ||| |||:|||
Db      61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT   5
Q9UL81
ID   Q9UL81      PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;


  Query Match             70.3%;  Score 395;  DB 4;  Length 107;
  Best Local Similarity   71.7%;  Pred. No. 6.7e-37;
  Matches   76;  Conservative   10;  Mismatches   20;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||||: || |: |: |||| ||||| |||:  |:|| |:|| |
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||| |:| ||| || || ||||| |  :  ||| ||||:|:
Db      61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106


RESULT   6
Q9UL79
ID   Q9UL79       PRELIMINARY;       PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;


  Query Match             68.6%;  Score 385.5;  DB 4;  Length 108;
  Best Local Similarity   72.0%;  Pred. No. 7.9e-36;
  Matches   77;  Conservative    8;  Mismatches   21;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           || |||||| |||| ||||||:|: || |: |:||||| ||||| |||:  | || |:||
Db       1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |:| ||| || || ||||| || :   ||||||||||
Db      61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107


RESULT   7
Q9R1A5
ID   Q9R1A5       PRELIMINARY;       PRT;   214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23922 MW;  52BA205FDE995E2A CRC64;


  Query Match             68.4%;  Score 384.5;  DB 11;  Length 214;
  Best Local Similarity   66.4%;  Pred. No. 2.3e-35;
  Matches   71;  Conservative   18;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:|||||: ||:|:|||||| ||||| |::|:|| |||:|: ||:  : |  |:||
Db       1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||||:||: |||||: ||:  |||||||    :||| |||:|||
Db      61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107


RESULT   8
Q91WS9
ID   Q91WS9       PRELIMINARY;       PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   233 AA;  25781 MW;  B1C184DA149A16EB CRC64;


  Query Match             67.5%;  Score 379.5;  DB 11;  Length 233;
  Best Local Similarity   69.2%;  Pred. No. 9.2e-35;
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  Matches   74;  Conservative   12;  Mismatches   20;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||: |||||:|||||:|  || |  |: |||| |    :|||:|||:|  |:||
Db      20 DIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 79

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| ||: |||:|:|||||||||| ||  | |||| |||:|||
Db      80 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIK 126


RESULT  9
Q96PF6
ID   Q96PF6       PRELIMINARY;      PRT;   116 AA.
AC   Q96PF6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN   SDNK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21361171; PubMed=11468171;
RA   Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT   "The tropism of organ involvement in primary systemic amyloidosis:
RT   contributions of Ig V(L) germ line gene use and clonal plasma cell
RT   burden.";
RL   Blood 98:714-720(2001).
DR   EMBL; AF361758; AAK51465.1; -.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12735 MW;  E796FC2217BFCF57 CRC64;


  Query Match             65.0%;  Score 365.5;  DB 4;  Length 116;
  Best Local Similarity   66.4%;  Pred. No. 1.5e-33;
  Matches   71;  Conservative   14;  Mismatches   21;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||  |: ||||  :: |||: ||:||: ||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTFICQASQDIANHLNWYQKKPGEAPKFLIYDGSFLKTGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| ||  ::| |||||||||| ||||| || :| :||| ||||: |
Db      61 RFSGGGSATNFTVTISSLQPEDFATYYCQQYHHLPFTFGPGTKVDFK 107


RESULT  10
Q9JL84
ID   Q9JL84       PRELIMINARY;      PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).

DR   EMBL; AF206022; AAF69320.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;


  Query Match             64.5%;  Score 362.5;  DB 11;  Length 107;
  Best Local Similarity   65.4%;  Pred. No. 3e-33;
  Matches   70;  Conservative   11;  Mismatches   25;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||| ||||||:|||   |  || |:   |:|| |    :|||:|||:|  |:||
Db       1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| ||: |||:|:|||||||||| ||   |||| |||:|||
Db      61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107


RESULT  11
Q91WF8
ID   Q91WF8       PRELIMINARY;      PRT;   234 AA.
AC   Q91WF8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 25.9 KDA PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015292; AAH15292.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25929 MW;  B0D0B0E6EB7812D2 CRC64;


  Query Match             63.3%;  Score 355.5;  DB 11;  Length 234;
  Best Local Similarity   64.5%;  Pred. No. 4.7e-32;
  Matches   69;  Conservative   17;  Mismatches   20;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||: ||||||:||||||:|: |||| |: |||| |    :|||:||| |  |:||
Db      21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
           ||||||||  ||: |||:|: |||||||:| | :   :||| |||:|:|
Db      81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK 127


RESULT  12
Q920E6
ID   Q920E6       PRELIMINARY;      PRT;   109 AA.
AC   Q920E6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
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RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307938; AAL09422.1; -.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11943 MW;  DAD3F98E05DD1501 CRC64;


  Query Match             62.9%;  Score 353.5;  DB 11;  Length 109;
  Best Local Similarity   61.7%;  Pred. No. 3.2e-32;
  Matches   66;  Conservative   16;  Mismatches   24;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||:|||||||: |||||: | :|: |:|||||  ||:|:||::    |  |:||
Db       1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
           ||||||||  |:  |:|||||  :|||  :    |||| |||:|||
Db      61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107


RESULT  13
Q9QYF0
ID   Q9QYF0       PRELIMINARY;      PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CN 8 SCFV.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RX   MEDLINE=20183931; PubMed=10706631;
RA   Shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a vascular cell wall-specific monoclonal antibody
RT   recognizing a cell polarity by using a phage display subtraction
RT   method.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;


  Query Match             60.1%;  Score 337.5;  DB 11;  Length 298;
  Best Local Similarity   58.9%;  Pred. No. 6.6e-30;
  Matches   63;  Conservative   19;  Mismatches   24;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||::||||:|||||||: |||||: | :|: |:|||||  ||:|:|||::    |  |:||
Db     173 DIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 232

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
           ||||||||  |:  |:|||||  :|||  :    :||| |||:|||
Db     233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279


RESULT  14
Q9UL83
ID   Q9UL83       PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;


  Query Match             59.9%;  Score 336.5;  DB 4;  Length 108;
  Best Local Similarity   60.2%;  Pred. No. 2.6e-30;
  Matches   65;  Conservative   17;  Mismatches   23;  Indels    3;  Gaps    2;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           :| |||||::|| | |:| |::|: || ::  :|||||  ||:|||||:  |    |||:
Db       1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
           |||||||| ::| |||||| || | |||  |:| |  ||| ||||:||
Db      61 RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107


RESULT  15
Q9UL85
ID   Q9UL85       PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;


  Query Match             59.1%;  Score 332;  DB 4;  Length 109;
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Best Local Similarity 61.5%; Pred. No. 8.4e-30;
Matches 67; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

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Db       1 EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW---TFGQGTKVEIK 106
           |||||||| ::| |||||| || | |:| || | |   ||| |||||||
Db      61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQY-NSWPPLTFGGGTKVEIK 108
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Search completed: July 9, 2002, 15:45:35
Job time: 386 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 ; Search time 51.18 Seconds
(without alignments)
230.047 Million cell updates/sec

Title: US-09-010-377-1
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	16	AAR81321	Humanized anti-VLA
2	562	100.0	106	18	AAW22412	Humanised alpha-4
3	562	100.0	126	18	AAW22419	Humanised alpha-4
4	508	90.4	106	16	AAR81328	Mouse anti-VLA-4 a
5	508	90.4	126	16	AAR81326	Mouse VLA-4 antibo
6	508	90.4	126	16	AAR81332	Human VLA-4 reshap
7	508	90.4	126	18	AAW22409	Alpha-4 integrin m
8	488	86.8	359	20	AAY29913	Human MCP-3 and mu
9	488	86.8	361	20	AAY29911	Human IP-10 and mu
10	488	86.8	374	20	AAY29916	Artificial synthet
11	481	85.6	128	15	AAR60627	MEI-14 light chain
12	475.5	84.6	234	12	AAR13050	CD4-specific CDR-g
13	471.5	83.9	107	16	AAR78970	Light chain variab
14	465	82.7	108	17	AAR93159	Murine monoclonal
15	460.5	81.9	128	11	AAR06252	Variable region of
16	460	81.9	637	13	AAR26983	(FRP51)-ETA fusion
17	456	81.1	109	19	AAW26797	Anti-gp54 MAb T16
18	455	81.0	240	16	AAR85495	ScFv(FWP51). Synt
19	455	81.0	241	20	AAY21882	Amino acid sequenc
20	455	81.0	245	19	AAW26800	Anti-gp54 MAb T16
21	453.5	80.7	107	16	AAR81322	Humanized VLA-4 an
22	453.5	80.7	107	18	AAW22422	Humanised alpha-4
23	453	80.6	109	12	AAR13658	Murine OKT4A light
24	452	80.4	241	13	AAR26981	FWP51 fusion prote
25	451.5	80.3	108	16	AAR65163	Human RE1 monoclon
26	451.5	80.3	129	15	AAR47207	Human/murine IL-1
27	451	80.2	355	18	AAW35133	R. pipiens recombi
28	449.5	80.0	107	19	AAW86805	Variable Light dom
29	449.5	80.0	107	19	AAW70625	Humanised murine a
30	446.5	79.4	108	18	AAW10231	CDR-grafted light
31	446.5	79.4	110	19	AAW70673	Anti-VEGF humanise
32	446.5	79.4	234	18	AAW10233	TF8-5G9 CDR-grafte
33	446.5	79.4	237	19	AAW70703	Protein encoded by
34	445.5	79.3	107	19	AAW86804	Variable Light dom
35	445.5	79.3	107	19	AAW70623	Humanised murine a
36	444.5	79.1	107	20	AAW87455	Humanised anti-alp
37	444.5	79.1	107	22	AAB62087	Human Vl consensus
38	444.5	79.1	107	22	AAB60400	Consensus human li
39	444.5	79.1	107	22	AAB61585	Human variable lig
40	444.5	79.1	108	19	AAW70622	Human consensus fr
41	444.5	79.1	108	21	AAY82345	Human consensus se
42	444.5	79.1	126	13	AAR29015	pUC-RV1-PM1a. Syn
43	444.5	79.1	126	13	AAR29013	pUC-RVh-PM1a. Syn
44	444.5	79.1	256	21	AAY55072	Interleukin-6 spec
45	444.5	79.1	260	21	AAY55075	Single chain Fv pr

ALIGNMENTS

RESULT 1
AAR81321
ID AAR81321 standard; Protein; 106 AA.
XX
AC AAR81321;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX

PS Claim 9; Page 67; 105pp; English.
XX
CC The sequence encodes the humanized mouse antibody 21.6 light chain
CC variable region, La, directed against leukocyte adhesion molecule
CC VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC AAQ99892) regions are linked to human constant regions in the
CC construction of a humanized antibody against VLA-4. The 5' and 3'
CC ends of the mouse cDNAs are modified using PCR primers (See
CC AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC containing human kappa or gamma-1 constant regions. In the humanized
CC light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC VR framework are replaced by the amino acid present in the equivalent
CC position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC antibodies are transfected into COS cells. The humanized antibodies
CC can be used for inhibiting adhesion of a leukocyte to an endothelial
CC cell and for treating inflammatory diseases such as multiple
CC sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can
CC also be used for detecting VLA-4, for affinity purification or for
CC generating anti-idiotype antibodies.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 562; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
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RESULT 2
AAW22412
ID AAW22412 standard; Protein; 106 AA.
XX
AC AAW22412;
XX
DT 08-DEC-1997 (first entry)
XX
DE Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW transplant rejection; graft versus host disease; nephritis;
KW atopic dermatitis; psoriasis; myocardial ischaemia;
KW acute leukocyte mediated lung injury; therapy.
XX
OS Chimeric Mus musculus;
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX

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FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Misc-difference 45
FT                   /note= "REI Lys-45 is substd. by Lys of mouse
FT                         21.6 VL, important in supporting the
FT                         CDR2 loop"
FT   Misc-difference 49
FT                   /note= "REI Tyr-49 is substd. by His of mouse
FT                         21.6 VL, located at the binding site"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Misc-difference 58
FT                   /note= "REI Val-58 is substd. by Ile of mouse
FT                         21.6 VL, important in supporting the CDR2
FT                         loop"
FT   Misc-difference 69
FT                   /note= "REI Thr-69 is substd. by Arg of mouse
FT                         21.6 VL, involved in antibody-antigen
FT                         binding"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "REI framework region 4"
FT   Misc-difference 103
FT                   /note= "REI Leu-103 substd. by Val, more typical
FT                         of human kappa light chain J region"
FT   Misc-difference 104
FT                   /note= "REI Gln-104 substd. by Glu, more typical
FT                         of human kappa light chain J region"
FT   Misc-difference 106
FT                   /note= "REI Thr-106 substd. by Lys, more typical
FT                         of human kappa light chain J region"
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XX
PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 25; Fig 6; 107pp; English.
XX
CC This polypeptide, designated La, comprises the light chain variable
CC region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC composed of complementarity determining regions (CDRs) from the VL
CC region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC 21.6 and a modified human REI framework. It can be expressed in
CC mammalian host cells following PCR amplification and mutagenesis
CC of appropriate fragments of mouse and human DNA sequences. The
CC humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC to produce a claimed humanised 21.6 antibody that is useful in the
CC manufacture of a medicament for treating asthma, atherosclerosis,
CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibody has a
CC half-life in the human circulation essentially equivalent to that
CC of naturally occurring human antibodies.
XX
SQ Sequence 106 AA;

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  Query Match             100.0%;  Score 562;  DB 18;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1e-36;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db      61 rfsgsgsgrdytftisslqpedIatyyclqydnlwtfgqgtkveik 106


RESULT   3
AAW22419
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Protein         21..126
FT                   /label= Mat_protein
FT                   /note= "VL version La (Claim 25)"
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "REI framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412).  It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;


  Query Match             100.0%;  Score 562;  DB 18;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-36;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      81 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 126


RESULT   4
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "mouse light chain variable framework
FT                   region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "mouse light chain variable framework
FT                   region 2"
FT   Region          50..56
FT                   /label= CDR2
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FT                   /note= "mouse light chain variable complementarity
FT                          determining region 2"
FT   Region          57..88
FT                   /label= FR3
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FT                          region 3"
FT   Region          89..96
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FT                   /note= "mouse light chain variable complementarity
FT                          determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "mouse light chain variable framework
FT                          region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;

  Query Match             90.4%;  Score 508;  DB 16;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:|||||||||||||||||| |||:|||
Db      61 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106


RESULT   5
AAR81326
ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;
```

```
  Query Match             90.4%;  Score 508;  DB 16;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.8e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||||||||||||||||  ||| ||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:|||||||||||||||||||| ||||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126


RESULT   6
AAR81332
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..20
FT                    /note= "signal peptide"
FT   Region           21..43
FT                    /note= "framework region 1"
FT   Region           44..54
FT                    /note= "complementarity determining region 1"
FT   Region           55..69
FT                    /note= "framework region 2"
FT   Region           70..76
FT                    /note= "complementarity determining region 2"
FT   Region           77..108
FT                    /note= "framework region 3"
FT   Region           109..116
FT                    /note= "complementarity determining region 3"
FT   Region           117..126
FT                    /note= "framework region 4"
FT
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions.  In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis.  They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis.  The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;

  Query Match             90.4%;  Score 508;  DB 16;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.8e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||||||||||||||||  ||| ||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:|||||||||||||||||||| ||||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126


RESULT   7
AAW22409
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..20
FT                    /label= Leader
FT   Region           21..43
FT                    /label= FR1
FT                    /note= "framework region 1"
FT   Region           44..54
FT                    /label= CDR1
FT                    /note= "complementarity determining region 1"
FT   Region           55..69
FT                    /label= FR2
FT                    /note= "framework region 2"
FT   Region           70..76
FT                    /label= CDR2
FT                    /note= "complementarity determining region 2"
FT   Region           77..108
FT                    /label= FR3
FT                    /note= "framework region 3"
FT   Region           109..116
FT                    /label= CDR3
FT                    /note= "complementarity determining region 3"
FT   Region           117..126
FT                    /label= FR4
FT                    /note= "framework region 4"
XX
```

PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
DR N-PSDB; AAT74759.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 18; Page 68; 107pp; English.
XX
CC This polypeptide comprises the light chain variable region (VL) of
CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC complementarity determining regions (CDRs) of the 21.6 VL can be
CC incorporated into a human REI framework to produce a claimed
CC humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC antibody that is used in the manufacture of a medicament for
CC treating a disease selected from asthma, atherosclerosis, AIDS,
CC dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibodies of the
CC invention have a half-life in the human circulation essentially
CC equivalent to that of naturally occurring human antibodies.
XX
SQ Sequence 126 AA;

Query Match 90.4%; Score 508; DB 18; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.8e-32;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:||||||||||||||||||||| |||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
```

RESULT 8
AAY29913
ID AAY29913 standard; Protein; 359 AA.
XX
AC AAY29913;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human MCP-3 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 118-119; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 359 AA;

Query Match 86.8%; Score 488; DB 20; Length 359;
Best Local Similarity 84.9%; Pred. No. 1.7e-30;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| ||||||:||||  ||| |||||||||| |||||||
Db     233 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 292

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:||:|:|||||||||||||||:||| |||:|||
Db     293 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338
```

RESULT 9
AAY29911
ID AAY29911 standard; Protein; 361 AA.
XX
AC AAY29911;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human IP-10 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 115-116; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 361 AA;

```
  Query Match             86.8%;  Score 488;  DB 20;  Length 361;
  Best Local Similarity   84.9%;  Pred. No. 1.7e-30;
  Matches   90;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             |||||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db     235 diqmtqspsslsaslggkvtitckasqdinkylawyqhkpgkgprllihytstlqpgips 294

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
             ||||||||||:|:||:|:|||||||||||||||:||| |||:|||
Db     295 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 340
```

RESULT 10
AAY29916
ID AAY29916 standard; Protein; 374 AA.
XX
AC AAY29916;
XX
DT 17-NOV-1999 (first entry)
XX
DE Artificial synthetic construct protein SEQ ID NO:15.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 117-118; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC or preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.
XX
SQ Sequence 374 AA;

```
  Query Match             86.8%;  Score 488;  DB 20;  Length 374;
  Best Local Similarity   84.9%;  Pred. No. 1.7e-30;
  Matches   90;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             |||||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db      95 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 154

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
             ||||||||||:|:||:|:|||||||||||||||:||| |||:|||
Db     155 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 200
```

RESULT 11
AAR60627
ID AAR60627 standard; Protein; 128 AA.
XX
AC AAR60627;
XX
DT 04-JUN-1995 (first entry)
XX
DE ME1-14 light chain variable region.
XX
KW Monoclonal antibody; tumour.
XX
OS Homo sapiens.
XX
PN WO9421294-A.
XX
PD 29-SEP-1994.
XX
PF 14-MAR-1994; 94WO-US02724.
XX
PR 19-MAR-1993; 93US-0033864.
XX
PA (BIGN/) BIGNER D D.
PA (CARR/) CARREL S.
PA (ZALU/) ZALUTSKY M R.
XX
PI Bigner DD, Carrel S, Zalutsky MR;
XX
DR WPI; 1994-316669/39.
DR N-PSDB; AAQ73537.
XX
PT Method of treating solid or cystic tumours with antibodies - by
PT administering monoclonal antibody Mel-14, having Fc deleted,

PT using injection or deposition in the cyst cavity
XX
PS Disclosure; Fig 2; 31pp; English.
XX
CC The sequence is that of the ME1-14 light chain. The protein is a
CC monoclonal antibody which can be administered to treat solid or
CC cystic tumours.
CC See also AAR60626.
XX
SQ Sequence 128 AA;

Query Match 85.6%; Score 481; DB 15; Length 128;
Best Local Similarity 84.0%; Pred. No. 2.3e-30;
Matches 89; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 21 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllmhytstlqpgips 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
Db 81 rfsgsgsgrdysfsisnlepediatyyclqydnlltfgggtkleik 126

RESULT 12
AAR13050
ID AAR13050 standard; Protein; 234 AA.
XX
AC AAR13050;
XX
DT 27-SEP-1991 (first entry)
XX
DE CD4-specific CDR-grafted light chain.
XX
KW variable region; antibody; OKT4A; heavy chain; CD4;
KW complementarity determining region.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal sequence
FT Region 21..45
FT /label= framework region 1
FT Region 46..52
FT /label= CDR 1
FT Region 53..69
FT /label= framework region 2
FT Region 70..76
FT /label= CDR 2
FT Region 77..110
FT /label= framework region 3
FT Region 111..116
FT /label= CDR 3
FT Region 117..132
FT /label= framework region 4
FT Region 133..234
FT /label= kappa constant domain
XX
PN WO9109966-A.
XX
PD 11-JUL-1991.
XX
PF 21-DEC-1990; 90WO-GB02015.
XX
PR 21-DEC-1989; 89GB-0028874.
PR 21-DEC-1990; 90WO-GB02017.
PR 21-DEC-1990; 90WO-GB02018.
XX
PA (ORTH) ORTHO PHARM CORP.
XX
PI Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
XX
DR WPI; 1991-222914/30.
DR N-PSDB; AAQ12633.
XX
PT New CD4 specific recombinant - complementarity determining region
PT grafted antibody for treating graft rejection and T cell
PT disorders
XX
PS Claim 1; Fig 8; 96pp; English.
XX
CC This is an example of a CDR-grafted light chain of the invention.
CC The constant regions are based on sequences of the human kappa
CC constant domain, the signal sequence is derived from murine MAb
CC B72.3 and the CDR sequences are based on the murine OKT4A light chain
CC CDRs. The recombinant antibody encoded by this sequence has affinity
CC for CD4 similar to that of OKT4A.
CC See also AAQ12627-Q12632.
XX
SQ Sequence 234 AA;

Query Match 84.6%; Score 475.5; DB 12; Length 234;
Best Local Similarity 84.9%; Pred. No. 1e-29;
Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 21 diqmtqspsslsasvgdrvtitckaspdinnylnwyqqtpgkapklliyytstlqpgvps 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
Db 81 rfsgsgsgteytftisslqpediatyycqqydnllftfgqgtklqi 126

RESULT 13
AAR78970
ID AAR78970 standard; Protein; 107 AA.
XX
AC AAR78970;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 23F8.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97508.
XX
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 23; Page 67-68; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate

CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAbs that were strongly positive
CC against glutatione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX
SQ Sequence 107 AA;

Query Match 83.9%; Score 471.5; DB 16; Length 107;
Best Local Similarity 83.2%; Pred. No. 1e-29;
Matches 89; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db       1 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
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Db      61 rfsggsgsgrdysfsisnpepediatyyclqydnslftfgsgtkleik 107
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RESULT 14
AAR93159
ID AAR93159 standard; Protein; 108 AA.
XX
AC AAR93159;
XX
DT 24-OCT-1996 (first entry)
XX
DE Murine monoclonal antibody K20 kappa chain variable region.
XX
KW Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW T cell activation; complementarity determining region; CDR.
XX
OS Mus musculus.
XX

FH	Key	Location/Qualifiers
FT	Region	1..23
FT		/label= FR1
FT		/note= "framework region"
FT	Region	24..34
FT		/label= CDR1
FT		/note= "complementarity determining region"
FT	Region	35..49
FT		/label= FR2
FT		/note= "framework region"
FT	Region	50..56
FT		/label= CDR2
FT		/note= "complementarity determining region"
FT	Region	57..88
FT		/label= FR3
FT		/note= "framework region"
FT	Region	89..94
FT		/label= CDR3
FT		/note= "complementarity determining region"
FT	Region	95..108
FT		/label= J_kappa1

XX
PN FR2724393-A1.
XX
PD 15-MAR-1996.
XX
PF 12-SEP-1994; 94FR-0010858.
XX
PR 12-SEP-1994; 94FR-0010858.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PROT-) PROTEINE PERFORMANCE SA.
XX
PI Bernard A, Cervoni MF, Lefranc MP, Margaritte C;
PI Poul MA;
XX
DR WPI; 1996-162083/17.
DR N-PSDB; AAT26849.
XX
PT Humanisation of non-human immunoglobulin variable regions - for
PT prodn. of humanised antibodies, esp. K20, e.g. as an
PT immunosuppressant
XX
PS Example 1; Fig 2A; 39pp; French.
XX
CC The present sequence is that of the variable region of the kappa
CC light chain from murine monoclonal antibody K20. The antibody
CC recognises the beta 1 subunit (CD29) of integrins and inhibits
CC activation and proliferation of peripheral T cells induced by
CC anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC for humanisation; the humanised version may be useful as an
CC immunosuppressant. In the humanisation process, the complementarity
CC determining regions (CDRs) of a human antibody with framework
CC regions 70-95% homologous to those of K20 were replaced by the K20
CC CDRs.
XX
SQ Sequence 108 AA;

Query Match 82.7%; Score 465; DB 17; Length 108;
Best Local Similarity 81.1%; Pred. No. 3.4e-29;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 15
AAR06252
ID AAR06252 standard; protein; 128 AA.
XX
AC AAR06252;
XX
DT 10-DEC-1990 (first entry)
XX
DE Variable region of murine AHT 107 light chain.
XX
KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS Mus sp.
XX
PN EP380068-A.
XX
PD 01-AUG-1990.
XX
PF 24-JAN-1990; 90EP-0101351.
XX

PR 04-DEC-1989; 89US-0441702.
PR 24-JAN-1989; 89US-0301216.
XX
PA (MOLE-) MOLECULAR THERAPEU.
XX
PI Zerler B;
XX
DR WPI; 1990-232892/31.
DR N-PSDB; AAQ05556.
XX
PT Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region
XX
PS Disclosure; ; p; English.
XX
CC MAbs comprising mouse CH and CL constant regions whith human
CC variable regions may be used to create mouse/human hybrid MAbs,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ Sequence 128 AA;

Query Match 81.9%; Score 460.5; DB 11; Length 128;
Best Local Similarity 76.6%; Pred. No. 8.8e-29;
Matches 82; Conservative 18; Mismatches 6; Indels 1; Gaps 1;

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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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Db      81 rfsgsqsgkdysfsinnlepediatyyclryddlpwtfgggtklevr 127
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Search completed: July 9, 2002, 15:40:36
Job time: 122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 ; Search time 20.73 Seconds
(without alignments)
124.897 Million cell updates/sec

Title: US-09-010-377-1
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	2	US-08-561-521-7	Sequence 7, Appli
2	562	100.0	106	5	PCT-US95-01219-7	Sequence 7, Appli
3	508	90.4	106	2	US-08-561-521-5	Sequence 5, Appli
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appli
5	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appli
6	508	90.4	126	2	US-08-561-521-15	Sequence 15, Appl
7	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appli
8	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appl
9	481	85.6	128	1	US-08-339-582-4	Sequence 4, Appli
10	471.5	83.9	107	2	US-08-888-366-22	Sequence 22, Appl
11	460	81.9	637	1	US-08-235-838-16	Sequence 16, Appl
12	460	81.9	637	2	US-08-465-473B-16	Sequence 16, Appl
13	455	81.0	241	1	US-08-235-838-11	Sequence 11, Appl
14	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appl
15	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appl
16	453.5	80.7	107	2	US-08-561-521-8	Sequence 8, Appli
17	453.5	80.7	107	5	PCT-US95-01219-8	Sequence 8, Appli
18	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appl
19	448.5	79.8	107	2	US-07-934-373C-17	Sequence 17, Appl
20	448.5	79.8	107	3	US-08-437-642B-17	Sequence 17, Appl
21	448.5	79.8	107	5	PCT-US93-07832-17	Sequence 17, Appl
22	444.5	79.1	107	2	US-07-934-373C-18	Sequence 18, Appl
23	444.5	79.1	107	3	US-08-437-642B-18	Sequence 18, Appl
24	444.5	79.1	107	5	PCT-US93-07832-18	Sequence 18, Appl
25	444.5	79.1	108	3	US-08-974-899-3	Sequence 3, Appli
26	444.5	79.1	111	1	US-08-137-117D-67	Sequence 67, Appl
27	444.5	79.1	111	2	US-08-436-717-67	Sequence 67, Appl
28	444.5	79.1	126	1	US-08-137-117D-71	Sequence 71, Appl
29	444.5	79.1	126	2	US-08-436-717-71	Sequence 71, Appl
30	443.5	78.9	107	2	US-08-561-521-6	Sequence 6, Appli
31	443.5	78.9	107	2	US-08-652-558-34	Sequence 34, Appl
32	443.5	78.9	107	4	US-09-025-203-15	Sequence 15, Appl
33	443.5	78.9	107	5	PCT-US95-01219-6	Sequence 6, Appli
34	443.5	78.9	108	2	US-08-070-116A-7	Sequence 7, Appli
35	443.5	78.9	108	2	US-08-116-247-9	Sequence 9, Appli
36	441.5	78.6	107	2	US-08-318-157B-6	Sequence 6, Appli
37	440.5	78.4	107	2	US-08-652-558-2	Sequence 2, Appli
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39	440.5	78.4	109	3	US-08-437-642B-3	Sequence 3, Appli
40	440.5	78.4	109	5	PCT-US93-07832-3	Sequence 3, Appli
41	440.5	78.4	214	2	US-07-934-373C-39	Sequence 39, Appl
42	440.5	78.4	214	3	US-08-437-642B-39	Sequence 39, Appl
43	440.5	78.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
44	438.5	78.0	107	4	US-09-254-189-1	Sequence 1, Appli
45	438.5	78.0	109	2	US-07-934-373C-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-7

Query Match 100.0%; Score 562; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;

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  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT   2
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
;  GENERAL INFORMATION:
;     APPLICANT:  Bendig, Mary M.
;     APPLICANT:  Leger, Olivier J.
;     APPLICANT:  Saldanha, Jose
;     APPLICANT:  Jones, S. Tarran
;     TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;     TITLE OF INVENTION:  Adhesion Molecule VLA-4
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/01219
;       FILING DATE:  25-JAN-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/186,269
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  106 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-01219-7


  Query Match             100.0%;  Score 562;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-45;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT   3
US-08-561-521-5
;
; Sequence 5, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;     APPLICANT:  Bendig, Mary M.
;     APPLICANT:  Leger, Olivier J.
;     APPLICANT:  Saldanha, Jose
;     APPLICANT:  Jones, S. Tarran
;     TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;     TITLE OF INVENTION:  Adhesion Molecule VLA-4
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/561,521
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,269A
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  106 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-561-521-5


  Query Match             90.4%;  Score 508;  DB 2;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.2e-40;
  Matches  94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

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Db       1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106


RESULT   4
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
;  GENERAL INFORMATION:
;     APPLICANT:  Bendig, Mary M.
;     APPLICANT:  Leger, Olivier J.
;     APPLICANT:  Saldanha, Jose
;     APPLICANT:  Jones, S. Tarran
;     TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;     TITLE OF INVENTION:  Adhesion Molecule VLA-4
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
```

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;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/01219
;       FILING DATE:  25-JAN-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/186,269
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  106 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-01219-5


  Query Match             90.4%;  Score 508;  DB 5;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.2e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:||||||||||||||||||||| |||:|||
Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106


RESULT   5
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-2


  Query Match             90.4%;  Score 508;  DB 2;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||||||||||||||  ||| ||||||||||||||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:||||||||||||||||||||| |||:|||
Db      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   6
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-15


  Query Match             90.4%;  Score 508;  DB 2;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   7
PCT-US95-01219-2
; Sequence 2, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-2


  Query Match             90.4%;  Score 508;  DB 5;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   8
PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-15


  Query Match             90.4%;  Score 508;  DB 5;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   9
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
;  GENERAL INFORMATION:
;    APPLICANT:  Bigner, Darell D.
;    APPLICANT:  Zalutsky, Michael R.
;    APPLICANT:  Carrel, Stefan
```

```
;    TITLE OF INVENTION:  METHOD OF TREATMENT
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5558852th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/339,582
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,864
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5405-89
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-339-582-4


  Query Match            85.6%;  Score 481;  DB 1;  Length 128;
  Best Local Similarity  84.0%;  Pred. No. 4.9e-38;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:|||| ||| ||||:|||| |||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||||||| ||| |||:|||
Db      81 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGGTKLEIK 126


RESULT  10
US-08-888-366-22
; Sequence 22, Application US/08888366
; Patent No. 5972656
;  GENERAL INFORMATION:
;    APPLICANT:  Lopez, Osvaldo
;    APPLICANT:  Wylie, Dwane E.
;    APPLICANT:  Wagner, Fred W.
;    TITLE OF INVENTION:  Mercury Binding Polypeptides and Nucleotides Coding Therefore
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 5972656west Ctr.
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,366
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/187,407
;      FILING DATE:  27-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,542
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/493,299
;      FILING DATE:  14-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/324,392
;      FILING DATE:  14-MAR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.39USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-888-366-22


  Query Match            83.9%;  Score 471.5;  DB 2;  Length 107;
  Best Local Similarity  83.2%;  Pred. No. 3.1e-37;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:|||| ||| ||||:|||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
           |||||||||||:|:||: :|||||||||||||| |:||| |||:|||
Db      61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107


RESULT  11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott.
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-838-16


  Query Match             81.9%;  Score 460;  DB 1;  Length 637;
  Best Local Similarity   80.2%;  Pred. No. 2.6e-35;
  Matches   85;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             |||:|||||||||||:|  |||||| |||| ||:||||  |||:|||||||||| |||||||
Db     168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:| :|:||||||||||| || |:||| |||:|||
Db     228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  12
US-08-465-473B-16
; Sequence 16, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-16


  Query Match             81.9%;  Score 460;  DB 2;  Length 637;
  Best Local Similarity   80.2%;  Pred. No. 2.6e-35;
  Matches   85;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             |||:|||||||||||:|  |||||| |||| ||:||||  |||:|||||||||| |||||||
Db     168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:| :|:||||||||||| || |:||| |||:|||
Db     228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  13
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  241 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-235-838-11


  Query Match             81.0%;  Score 455;  DB 1;  Length 241;
  Best Local Similarity   80.0%;  Pred. No. 2.6e-35;
  Matches   84;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:||||||||||:|  |||||| |||| ||:||||  |||:|||||||| |||||||
Db     137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
           |||||||||||:|:| :|:||||||||||| || |:||| |||:||
Db     197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  14
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  241 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-11


  Query Match             81.0%;  Score 455;  DB 2;  Length 241;
  Best Local Similarity   80.0%;  Pred. No. 2.6e-35;
  Matches   84;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:||||||||||:|  |||||| |||| ||:||||  |||:|||||||| |||||||
Db     137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
           |||||||||||:|:| :|:||||||||||| || |:||| |||:||
Db     197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  15
US-08-602-725-29
; Sequence 29, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Hukan REI light chain
US-08-602-725-29


  Query Match             80.9%;  Score 454.5;  DB 2;  Length 108;
  Best Local Similarity   83.0%;  Pred. No. 1.2e-35;
  Matches   88;  Conservative    8;  Mismatches    9;  Indels    1;  Gaps    1;
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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||||: |||| ||:||||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLAWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           |||||||| |||||||||||||||||| || :| :|||||||:||
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKIEI 106
```

Search completed: July 9, 2002, 15:39:04
Job time: 30 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:38 ; Search time 28.27 Seconds
(without alignments)
418.075 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488.5	74.6	178	2	S29594	Ig gamma chain (WM
2	477	72.8	120	2	S03471	Ig heavy chain V r
3	473.5	72.3	118	2	S36265	Ig heavy chain V-1
4	468	71.5	123	2	D33548	Ig heavy chain V r
5	467	71.3	142	2	A32483	Ig heavy chain V r
6	465	71.0	117	2	S17586	Ig heavy chain V r
7	459.5	70.2	122	2	S06823	Ig heavy chain V r
8	456.5	69.7	132	2	PH0954	Ig gamma chain V r
9	455	69.5	116	2	S24289	Ig gamma-1 chain -
10	455	69.5	221	2	S49220	Ig heavy chain V r
11	450	68.7	129	2	S46393	Ig heavy chain V-D
12	449	68.5	115	2	S03482	anti-Sm antibody V
13	447.5	68.3	135	2	S49530	Ig heavy chain V-D
14	447	68.2	120	2	S03484	Ig heavy chain V r
15	446.5	68.2	136	2	PH0960	Ig heavy chain pre
16	444	67.8	136	2	S04576	Ig heavy chain V r
17	443	67.6	119	2	PH0961	Ig heavy chain V r
18	441.5	67.4	268	2	A56446	Ig heavy chain V r
19	439.5	67.1	104	2	PH1665	nitrophenyl phosph
20	439.5	67.1	114	4	A47271	Ig heavy chain V-1
21	439	67.0	133	2	C33548	Ig mu chain precur
22	439	67.0	627	2	S14683	Ig heavy chain V r
23	438.5	66.9	114	2	PH1667	Ig heavy chain V r
24	438.5	66.9	118	2	PH1666	Ig heavy chain V r
25	437.5	66.8	137	2	S52445	Ig heavy chain V r
26	436.5	66.6	120	2	S31999	Ig heavy chain V r
27	435.5	66.5	120	2	PH0962	Ig heavy chain V r
28	435.5	66.5	128	2	PH0952	Ig heavy chain V-1
29	433.5	66.2	126	2	B33548	
30	433	66.1	127	2	PH0955	Ig heavy chain V r
31	433	66.1	135	2	PH0953	Ig heavy chain V r
32	431	65.8	126	2	I44151	Ig heavy chain V r
33	429.5	65.6	108	2	PH1012	Ig heavy chain V r
34	429	65.5	125	2	PH0957	Ig heavy chain pre
35	427.5	65.3	143	1	E1HUND	Ig heavy chain V r
36	427	65.2	125	2	S68170	Ig heavy chain V-1
37	427	65.2	129	2	A33548	Ig heavy chain V r
38	426	65.0	127	2	S34014	Ig heavy chain V r
39	425	64.9	129	2	S36260	Ig heavy chain V r
40	424.5	64.8	147	2	PH1561	Ig heavy chain V r
41	424.5	64.8	171	2	S23623	Ig gamma chain - m
42	421	64.3	246	2	S38950	Ig gamma-2a chain
43	421	64.3	446	2	S40295	Ig heavy chain V r
44	420.5	64.2	122	2	PH1426	Ig heavy chain V r
45	420	64.1	121	2	S20783	

ALIGNMENTS

RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match 74.6%; Score 488.5; DB 2; Length 178;
Best Local Similarity 75.6%; Pred. No. 1.2e-36;
Matches 93; Conservative 11; Mismatches 14; Indels 5; Gaps 2;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||:|||:| | | |||:||||||||||:|
Db      14 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANGYTEY 73

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||: ||||||| :|||::|||| |||||||||      |||  | |||||||| ||
Db      74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYWGQGTSVT 128

Qy     121 VSS 123
           |||
Db     129 VSS 131
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RESULT 2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982

```
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             72.8%;  Score 477;  DB 2;  Length 120;
  Best Local Similarity   75.6%;  Pred. No. 8.7e-36;
  Matches   93;  Conservative   11;  Mismatches   15;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||:|||:| | | |||:|||||||| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| |||||||::|||::|||| |||||||||||     |     |||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT   3
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             72.3%;  Score 473.5;  DB 2;  Length 118;
  Best Local Similarity   76.2%;  Pred. No. 1.8e-35;
  Matches   96;  Conservative    6;  Mismatches   13;  Indels   11;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||:    |:||||||||| ||||| |:| :| | | |
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
           |||||||| |||||||||||||||||||||||||||:   ||        :|||||||
Db      61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY--------LDYWGQGT 112

Qy     118 LVTVSS 123
           ||||||
Db     113 LVTVSS 118


RESULT   4
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

A;Reference number: A33548; MUID:89345575
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             71.5%;  Score 468;  DB 2;  Length 123;
  Best Local Similarity   74.8%;  Pred. No. 5.7e-35;
  Matches   92;  Conservative    7;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||:|||:     |:|||||||| ||||| |:| :| | |
Db       1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||| ||| :|||||||| |||:|||||||||  | | |     |||||||||||
Db      61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFFDYWGQGTLVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123


RESULT   5
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89273586
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>


  Query Match             71.3%;  Score 467;  DB 2;  Length 142;
  Best Local Similarity   73.2%;  Pred. No. 8.1e-35;
  Matches   93;  Conservative    8;  Mismatches   22;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||:    |:|||||||| ||||| |:|:   | |
Db      11 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSGNSTNY 70

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----GYYGNYGVYAMDYWGQG 116
           ||||||||:| ||| || |||||||||||||||||||      :|   :  |||||||
Db      71 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy     117 TLVTVSS 123
           |||||||
Db     131 TLVTVSS 137


RESULT   6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
```

forms.
A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 465; DB 2; Length 117;
Best Local Similarity 72.6%; Pred. No. 1e-34;
Matches 90; Conservative 15; Mismatches 11; Indels 8; Gaps 3;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| |||||||||:|||:| | : |||:|||||||:| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
           ||||| : |||||||::|||::|||| |||||||||| || |||:     ||||||| :
Db      61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy     120 TVSS 123
           ||||
Db     114 TVSS 117
```

RESULT 7
S06823
Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 70.2%; Score 459.5; DB 2; Length 122;
Best Local Similarity 73.4%; Pred. No. 3.2e-34;
Matches 91; Conservative 13; Mismatches 17; Indels 3; Gaps 3;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
           :||| |||||: |||||||:|| ||||||||||:| ||:| | | |||:|||||||| ||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy      60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLV 119
           ||||||||: |||||||::|||::|||| |||||||||| ||:       :|||||||| |
Db      61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy     120 TVSS 123
           ||||
Db     119 TVSS 122
```

RESULT 8
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

Query Match 69.7%; Score 456.5; DB 2; Length 132;
Best Local Similarity 72.0%; Pred. No. 6.5e-34;
Matches 95; Conservative 1; Mismatches 27; Indels 9; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||:|||||||||||       | |||||||| ||||| | |  |   |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR---------EGYYGNYGVYAMD 111
             |||||||||||| | |||||||||||||||||||||||          ||| ||  | ||
Db      61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120

Qy     112 YWGQGTLVTVSS 123
           ||||| |||||
Db     121 VWGQGTTVTVSS 132
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RESULT 9
S24289
Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 455; DB 2; Length 116;
Best Local Similarity 71.5%; Pred. No. 7.7e-34;
Matches 88; Conservative 13; Mismatches 14; Indels 8; Gaps 2;

```
Qy       2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
           ||| :|||: |||||||:|| || |||:|||:||||| | | |||:|||||||| | :|
Db       1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy      62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
           |||||: |||||||::|||::|||| ||||||||||  |||         ||||||| :|
Db      61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY-------FDYWGQGTTLT 113

Qy     121 VSS 123
           |||
Db     114 VSS 116
```

RESULT 10
S49220

Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 455; DB 2; Length 221;
Best Local Similarity 70.7%; Pred. No. 1.5e-33;
Matches 87; Conservative 12; Mismatches 20; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db 1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
Db 61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116

Qy 121 VSS 123
Db 117 VSS 119

RESULT 11
S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 450; DB 2; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.4e-33;
Matches 91; Conservative 10; Mismatches 22; Indels 6; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
Db 61 AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120

Qy 115 QGTLVTVSS 123
Db 121 KGTTVTVSS 129

RESULT 12
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03482
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 449; DB 2; Length 115;
Best Local Similarity 70.2%; Pred. No. 2.6e-33;
Matches 85; Conservative 12; Mismatches 18; Indels 6; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db 1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
Db 61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114

Qy 121 V 121
Db 115 V 115

RESULT 13
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 447.5; DB 2; Length 135;
Best Local Similarity 72.8%; Pred. No. 4.2e-33;
Matches 91; Conservative 7; Mismatches 16; Indels 11; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

```
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC--AREGYYGNYGVYAMDYWGQGTL 118
           |||||||:| ||| |||||||| |||:|||||||  || ||           :|||||||
Db      80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARARTGY---------NYWGQGTL 130

Qy     119 VTVSS 123
           |||||
Db     131 VTVSS 135


RESULT  14
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match           68.2%;  Score 447;  DB 2;  Length 120;
  Best Local Similarity  71.5%;  Pred. No. 4.2e-33;
  Matches   88;  Conservative   11;  Mismatches   20;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||:|||:| | | |||:|||||||  :||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||  |||||||:| ||::|||| | ||||||| |    | :   |||||||| ||
Db      61 GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  15
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3


  Query Match           68.2%;  Score 446.5;  DB 2;  Length 136;
  Best Local Similarity  69.1%;  Pred. No. 5.3e-33;
  Matches   94;  Conservative    1;  Mismatches   28;  Indels   13;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||:|||||||||          | |||||||| ||||| | |  |  |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR------------EGYYGNYGV 107
           |||||||||||| | ||||||||||||||||||||||||||          |||   |
Db      61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120

Qy     108 YAMDYWGQGTLVTVSS 123
           | || ||||| |||||
Db     121 YGMDVWGQGTTVTVSS 136


Search completed: July  9, 2002, 15:39:38
Job time: 64 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:45:57 ; Search time 15.81 Seconds
(without alignments)
301.234 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	427.5	65.3	147	1	HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1	HV03_MOUSE	P01747 mus musculu
3	408.5	62.4	139	1	HV07_MOUSE	P01751 mus musculu
4	405	61.8	117	1	HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1	HV02_MOUSE	P01746 mus musculu
6	396	60.5	117	1	HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1	HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1	HV13_MOUSE	P01757 mus musculu
9	375.5	57.3	118	1	HV51_MOUSE	P06330 mus musculu
10	373	56.9	117	1	HV12_MOUSE	P01756 mus musculu
11	371.5	56.7	137	1	HV11_MOUSE	P01755 mus musculu
12	369	56.3	138	1	HV48_MOUSE	P03980 mus musculu
13	364.5	55.6	120	1	HV50_MOUSE	P06329 mus musculu
14	360	55.0	121	1	HV01_MOUSE	P01745 mus musculu
15	360	55.0	136	1	HV15_MOUSE	P01759 mus musculu
16	355	54.2	125	1	HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1	HV1H_HUMAN	P80421 homo sapien
18	349	53.3	117	1	HV09_MOUSE	P01753 mus musculu
19	344.5	52.6	114	1	HV00_MOUSE	P01741 mus musculu
20	338	51.6	117	1	HV04_MOUSE	P01748 mus musculu
21	336	51.3	117	1	HV06_MOUSE	P01750 mus musculu
22	333.5	50.9	136	1	HV16_MOUSE	P01783 mus musculu
23	333	50.8	117	1	HV10_MOUSE	P01754 mus musculu
24	330.5	50.5	124	1	HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1	HV14_MOUSE	P01758 mus musculu
26	329	50.2	117	1	HV49_MOUSE	P06328 mus musculu
27	326	49.8	117	1	HV52_MOUSE	P06327 mus musculu
28	326	49.8	123	1	HV24_MOUSE	P01793 mus musculu
29	325.5	49.7	119	1	HV37_MOUSE	P01807 mus musculu
30	325.5	49.7	124	1	HV1D_HUMAN	P01760 homo sapien
31	324.5	49.5	119	1	HV38_MOUSE	P01808 mus musculu
32	323.5	49.4	119	1	HV40_MOUSE	P01810 mus musculu
33	320.5	48.9	122	1	HV3G_HUMAN	P01768 homo sapien
34	319	48.7	117	1	HV42_MOUSE	P01812 mus musculu
35	318.5	48.6	122	1	HV3A_HUMAN	P01762 homo sapien
36	318	48.5	121	1	HV3J_HUMAN	P01771 homo sapien
37	317	48.4	123	1	HV19_MOUSE	P01788 mus musculu
38	315	48.1	123	1	HV18_MOUSE	P01787 mus musculu
39	314.5	48.0	122	1	HV21_MOUSE	P01790 mus musculu
40	314	47.9	117	1	HV05_MOUSE	P01749 mus musculu
41	313	47.8	123	1	HV25_MOUSE	P01794 mus musculu
42	313	47.8	142	1	HV01_RAT	P01805 rattus norv
43	312	47.6	118	1	HV39_MOUSE	P01809 mus musculu
44	312	47.6	123	1	HV22_MOUSE	P01791 mus musculu
45	311.5	47.6	122	1	HV3H_HUMAN	P01769 homo sapien

ALIGNMENTS

```
RESULT   1
HV1C_HUMAN
ID   HV1C_HUMAN      STANDARD;      PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02026; E1HUND.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21       T -> V (IN REF. 2).
FT   CONFLICT     53     54       IH -> HI (IN REF. 2).
FT   CONFLICT     67     68       VG -> GV (IN REF. 2).
FT   CONFLICT    125    125       MISSING (IN REF. 2).
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  16491 MW;  948F9F72A5366C20 CRC64;

  Query Match          65.3%;  Score 427.5;  DB 1;  Length 147;
  Best Local Similarity  64.1%;  Pred. No. 6.3e-36;
  Matches   82;  Conservative   16;  Mismatches   25;  Indels    5;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           | |||||||||:||||||:|||||||:   |:||||:|||||  |||:| |:| :| | |
Db      20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ 115
```

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          |:|||||||:| | | |||||:| ||||:|:||:|||:       ||     | :| |||
Db      80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139

Qy     116 GTLVTVSS 123
           || |||||
Db     140 GTTVTVSS 147


RESULT   2
HV03_MOUSE
ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;


  Query Match             62.4%;  Score 409;  DB 1;  Length 120;
  Best Local Similarity   63.1%;  Pred. No. 3.5e-34;
  Matches   77;  Conservative   18;  Mismatches   25;  Indels    2;  Gaps    1;

Qy       2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
           ||| ||||| : :|:|||:|||||:        |:||:| ||| |||:| |:| |||||||:
Db       1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy      62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTV 121
           ||:|: |:| | |:|||||:| || |||:|||:||| ||| | | |||||||  :||
Db      61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLTV 118

Qy     122 SS 123
           ||
Db     119 SS 120


RESULT   3
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN      20     49       FRAMEWORK-1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      55     68       FRAMEWORK-2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      86    117       FRAMEWORK-3.
FT   DOMAIN     118    124       D SEGMENT.
FT   DOMAIN     125    139       JH2 SEGMENT.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;


  Query Match             62.4%;  Score 408.5;  DB 1;  Length 139;
  Best Local Similarity   62.6%;  Pred. No. 4.7e-34;
  Matches   77;  Conservative   18;  Mismatches   25;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: ||||||:|||||:     ::|||:| ||: |||:|||| :| |||
Db      20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :|||||:|||| ||||:|||||  |||:      |||||| :|
Db      80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT 136

Qy     121 VSS 123
           |||
Db     137 VSS 139


RESULT   4
HV1B_HUMAN
ID   HV1B_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
```

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RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION HG3.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12946 MW;  2D3F92FC60CD1FE7 CRC64;


  Query Match           61.8%;  Score 405;  DB 1;  Length 117;
  Best Local Similarity  79.6%;  Pred. No. 8.6e-34;
  Matches   78;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||:     |:|||||||||| ||||| |:|: | | |
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
           |||||||:| ||| || ||||||||||||||||||||
Db      80 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT   5
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    140       IG HEAVY CHAIN V REGION 93G7.
FT   NON_TER    140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;


  Query Match           60.9%;  Score 399;  DB 1;  Length 140;
  Best Local Similarity  61.0%;  Pred. No. 4.2e-33;
  Matches   75;  Conservative   19;  Mismatches   27;  Indels    2;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: : |:|||:|||||||:       |:|:|:| ||| |||:| |:| |||  |
Db      20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:||||||:| || |||:|||:|||  |||  | |  |||||| :|
Db      80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYG--GSYDFDYWGQGTPLT 137

Qy     121 VSS 123
           |||
Db     138 VSS 140


RESULT   6
HV1G_HUMAN
ID   HV1G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION V35.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  13009 MW;  BE61CE63F8CE97BD CRC64;


  Query Match           60.5%;  Score 396;  DB 1;  Length 117;
  Best Local Similarity  78.6%;  Pred. No. 6.8e-33;
  Matches   77;  Conservative    5;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
```

```
          ||||||||||||||||||||||||||:     |:|||||||||| |||||||:| :| | |
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
           ||||||| | ||| |||||||| |||:|| ||||||
Db      80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117


RESULT   7
HV1A_HUMAN
ID   HV1A_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01742;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC       MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR   PIR; A02023; G1HUEU.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12472 MW;  99D60ADAEBD52818 CRC64;


  Query Match             59.5%;  Score 390;  DB 1;  Length 117;
  Best Local Similarity   68.3%;  Pred. No. 2.7e-32;
  Matches   84;  Conservative    8;  Mismatches   25;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:||||||||||     : | ||||||| ||||| | |  |   |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             |||||||||| | :|||||||||||||||| |:||     | ||:|:  : :   | |||
Db      61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117


RESULT   8
HV13_MOUSE
ID   HV13_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;


  Query Match             57.7%;  Score 378;  DB 1;  Length 117;
  Best Local Similarity   58.5%;  Pred. No. 4.3e-31;
  Matches   72;  Conservative   20;  Mismatches   25;  Indels    6;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:   | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:||||||:|:|| |||:|||||||: |      :  | || || ||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------WYFDVWGAGTTVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117


RESULT   9
HV51_MOUSE
ID   HV51_MOUSE     STANDARD;      PRT;   118 AA.
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02040; MHMS38.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98       V SEGMENT.
FT   DOMAIN       99    104       D SEGMENT.
FT   DOMAIN      105    118       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
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FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  12934 MW;  94F7BEE4C762A018 CRC64;


  Query Match             57.3%;  Score 375.5;  DB 1;  Length 118;
  Best Local Similarity   58.5%;  Pred. No. 7.7e-31;
  Matches   72;  Conservative   17;  Mismatches   29;  Indels    5;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:    | |::|:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|   |||| || |||:|||||||       ||    | || || ||
Db      61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR-----GYGYDPFDVWGTGTTVT 115

Qy     121 VSS 123
           |||
Db     116 VSS 118


RESULT  10
HV12_MOUSE
ID   HV12_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01756;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83075344; PubMed=6816276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC       PROTEIN HAS ALSO BEEN DETERMINED.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A02039; MHMS4E.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   DISULFID     22     96       BY SIMILARITY.
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .).
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12983 MW;  3CF8ACE4BE447E41 CRC64;


  Query Match             56.9%;  Score 373;  DB 1;  Length 117;
  Best Local Similarity   59.3%;  Pred. No. 1.4e-30;
  Matches   73;  Conservative   19;  Mismatches   25;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:    | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|||||:|:|| |||:|||||||:     |  | | || || ||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD-----YDWY-FDVWGAGTTVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117


RESULT  11
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
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CC   ---------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;


  Query Match             56.7%;  Score 371.5;  DB 1;  Length 137;
  Best Local Similarity   60.2%;  Pred. No. 2.3e-30;
  Matches   74;  Conservative   14;  Mismatches   30;  Indels    5;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||  |||||||:|||||:       :||| | ||: |||:||||| :| | |
Db      20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           :  |: : |:| |  :|||||:|||| |||:|||||||     | |      ||||||| :|
Db      80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134

Qy     121 VSS 123
           |||
Db     135 VSS 137


RESULT  12
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
```

```
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      128    138       FRAMEWORK-4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;


  Query Match             56.3%;  Score 369;  DB 1;  Length 138;
  Best Local Similarity   58.1%;  Pred. No. 4.1e-30;
  Matches   72;  Conservative   20;  Mismatches   26;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||::|||||    : :||||:| ||| |||:| |:| :| : |
Db      20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV 119
           : ||: : |:| | |:||||||:|||  |: |||||| :|||  :       ||||||||
Db      80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF-----VYWGQGTLV 134

Qy     120 TVSS 123
           | |:
Db     135 TFSA 138


RESULT  13
HV50_MOUSE
ID   HV50_MOUSE      STANDARD;       PRT;   120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MHMS15.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98       V SEGMENT.
FT   DOMAIN       99    105       D SEGMENT.
FT   DOMAIN      106    120       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13311 MW;  914453F426F09834 CRC64;


  Query Match             55.6%;  Score 364.5;  DB 1;  Length 120;
  Best Local Similarity   56.1%;  Pred. No. 9.8e-30;
  Matches   69;  Conservative   19;  Mismatches   32;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||:| | |: |||||| :|||||:     ::||:|| ||| |||:| |:|:|| | |
Db       1 QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGGINPSNGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| | |:|  |||:||:  |||:|||||||  | |:       | || || ||
Db      61 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWDYEGD---RYFDVWGTGTTVT 117

Qy     121 VSS 123
           |||
Db     118 VSS 120


RESULT  14
HV01_MOUSE
ID   HV01_MOUSE      STANDARD;       PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
DR   PIR; A02027; GVMS11.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;


  Query Match             55.0%;  Score 360;  DB 1;  Length 121;
  Best Local Similarity   55.3%;  Pred. No. 2.8e-29;
  Matches   68;  Conservative   23;  Mismatches   30;  Indels    2;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           : || |||||: :|| |||:||||:|:   : :| ||:: ||  |||:| | |  |:| |
Db       1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60
```

```
Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           :   :|: |:||||||:||||::|||| |||:|:|:||| | | |   |  | ||||| :|
Db      61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT 118

Qy     121 VSS 123
           |||
Db     119 VSS 121


RESULT  15
HV15_MOUSE
ID   HV15_MOUSE      STANDARD;       PRT;   136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region BCL1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC   ---------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;


  Query Match             55.0%;  Score 360;  DB 1;  Length 136;
  Best Local Similarity   56.9%;  Pred. No. 3.2e-29;
  Matches   70;  Conservative   17;  Mismatches   30;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| ||| || :|| |||:||| ||:   |  :|||:|:  : |||:| |   | | | |
Db      20 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|| :|||: | ||||:|  ||||  |||||    |||||||  :|
Db      80 NQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--YYGNY----FDYWGQGTTLT 133

Qy     121 VSS 123
           |||
Db     134 VSS 136


Search completed: July  9, 2002, 15:45:57

Job time: 373 sec
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:45:35 ; Search time 43.02 Seconds
(without alignments)
494.616 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	457.5	69.8	124	4	Q9UL92	Q9ul92 homo sapien
2	440.5	67.3	159	4	Q96QS0	Q96qs0 homo sapien
3	440	67.2	468	11	Q99L31	Q99131 mus musculu
4	432	66.0	109	11	Q9JL85	Q9jl85 mus musculu
5	432	66.0	119	4	Q9UL94	Q9ul94 homo sapien
6	432	66.0	614	4	Q96GA6	Q96ga6 homo sapien
7	428	65.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
8	428	65.3	125	4	Q9UL95	Q9ul95 homo sapien
9	427	65.2	146	11	Q924Q3	Q924q3 mus musculu
10	422	64.4	473	11	Q9D8L4	Q9d8l4 mus musculu
11	415.5	63.4	145	11	Q924R4	Q924r4 mus musculu
12	415.5	63.4	145	11	Q924R1	Q924r1 mus musculu
13	412	62.9	146	11	Q924R8	Q924r8 mus musculu
14	411.5	62.8	116	4	Q9UL89	Q9ul89 homo sapien
15	409.5	62.5	145	11	Q924Q6	Q924q6 mus musculu
16	408.5	62.4	145	11	Q924Q7	Q924q7 mus musculu
17	408.5	62.4	473	11	Q99L25	Q99125 mus musculu
18	408	62.3	142	11	Q924Q1	Q924q1 mus musculu
19	407.5	62.2	143	11	Q924P9	Q924p9 mus musculu
20	407	62.1	117	11	Q9QXE9	Q9qxe9 mus musculu
21	405.5	61.9	145	11	Q924Q9	Q924q9 mus musculu
22	405	61.8	140	11	Q924R2	Q924r2 mus musculu
23	403.5	61.6	143	11	Q924R0	Q924r0 mus musculu
24	403.5	61.6	145	11	Q924P7	Q924p7 mus musculu
25	399	60.9	142	11	Q924Q2	Q924q2 mus musculu
26	399	60.9	150	4	Q9Y298	Q9y298 homo sapien
27	398.5	60.8	500	4	Q9BRV0	Q9brv0 homo sapien
28	398	60.8	481	11	Q91WT1	Q91wt1 mus musculu
29	394.5	60.2	143	11	Q924R7	Q924r7 mus musculu
30	393.5	60.1	145	11	Q924R3	Q924r3 mus musculu
31	391.5	59.8	488	11	Q91WR1	Q91wr1 mus musculu
32	389.5	59.5	137	11	Q924R6	Q924r6 mus musculu
33	389.5	59.5	143	11	Q91VA2	Q91va2 mus musculu
34	388.5	59.3	139	11	Q924R5	Q924r5 mus musculu
35	388.5	59.3	141	11	Q924Q4	Q924q4 mus musculu
36	386.5	59.0	118	11	Q9Z1C4	Q9z1c4 mus musculu
37	386	58.9	117	11	Q9QXF0	Q9qxf0 mus musculu
38	384	58.6	157	4	O95978	O95978 homo sapien
39	381.5	58.2	143	11	Q91V67	Q91v67 mus musculu
40	381.5	58.2	463	11	Q99LC4	Q991c4 mus musculu
41	381	58.2	146	11	Q924Q8	Q924q8 mus musculu
42	380.5	58.1	143	11	Q924Q5	Q924q5 mus musculu
43	380	58.0	144	11	Q924P5	Q924p5 mus musculu
44	380	58.0	484	11	Q99LA6	Q991a6 mus musculu
45	379.5	57.9	109	11	Q9JL75	Q9jl75 mus musculu

ALIGNMENTS

```
RESULT   1
Q9UL92
ID   Q9UL92       PRELIMINARY;       PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;

  Query Match           69.8%;  Score 457.5;  DB 4;  Length 124;
  Best Local Similarity 69.5%;  Pred. No. 3.8e-41;
  Matches   91;  Conservative    9;  Mismatches   16;  Indels   15;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||||:|||||||||||||||||:     |:|||||||| ||||| |:|: | | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
```

```
Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM--------DY 112
           |||||||:| ||| || ||||||||||||||||||||          |:| :         ||
Db      61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR-------GLYVVVPAAFSRFDY 113

Qy     113 WGQGTLVTVSS 123
           ||||||||||
Db     114 WGQGTLVTVSS 124
```

RESULT 2
Q96QS0
ID Q96QS0 PRELIMINARY; PRT; 159 AA.
AC Q96QS0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 67.3%; Score 440.5; DB 4; Length 159;
Best Local Similarity 64.9%; Pred. No. 3.4e-39;
Matches 87; Conservative 13; Mismatches 19; Indels 15; Gaps 2;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||:   : |::|||||||| |||| |:|: |  :|
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----------GYYGNYGVYA 109
           |||||:|:| ||| || ||:|||||:|||||:|||||          |:|     |
Db      80 SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFY----YYG 135

Qy     110 MDYWGQGTLVTVSS 123
           || ||||| ||||||
Db     136 MDVWGQGTTVTVSS 149
```

RESULT 3
Q99L31
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060O09 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 67.2%; Score 440; DB 11; Length 468;
Best Local Similarity 67.5%; Pred. No. 1.5e-38;
Matches 83; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: :|||||||:|| |||||||||: :|||:| | | ||||:| ||| :| |||
Db      20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||| : |||||||::|||::|||| |||||:|||||   || |     ||||||| :|
Db      80 APKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLLYGGY----YDYWGQGTTIT 135

Qy     121 VSS 123
           |||
Db     136 VSS 138
```

RESULT 4
Q9JL85
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 66.0%; Score 432; DB 11; Length 109;
Best Local Similarity 68.7%; Pred. No. 1.7e-38;
Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1;

```
Qy       9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
           ||: ||||||:|| |||||:|||:|||: | | |||:|||||| |::|||||||:
Db       1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy      69 TITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
           |||:|||::|||::|||| |||||||| |       |    |||||| :||||
Db      61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR------GAVVFDYWGQGTALTVSS 109
```

RESULT 5
Q9UL94

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ID   Q9UL94      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL94;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035020; AAD56256.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    119    119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F5345F4A16E CRC64;

  Query Match             66.0%;  Score 432;  DB 4;  Length 119;
  Best Local Similarity   70.7%;  Pred. No. 1.9e-38;
  Matches   87;  Conservative   10;  Mismatches   22;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :|||||:|||||||||||||||||||||:      |:|||||||| ||||| |:| :  | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||:||:| ||| |||||||| |||:|||||||||| |  | :     | ||||||||
Db      61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT   6
Q96GA6
ID   Q96GA6      PRELIMINARY;      PRT;   614 AA.
AC   Q96GA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:15420).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009851; AAH09851.1; -.
SQ   SEQUENCE   614 AA;  67921 MW;  55EF536E77AA9BBB CRC64;

  Query Match             66.0%;  Score 432;  DB 4;  Length 614;
  Best Local Similarity   71.5%;  Pred. No. 1.5e-37;
  Matches   88;  Conservative    9;  Mismatches   24;  Indels    2;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |:|||||||||||| |:|||||||||:      |:|||||||| ||||| | | || | |
Db      20 QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||| ||||| | | :|||||||||||||||:||||| ||  ::   | | |||||:||
Db      80 AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR-GYSSSWD-DAFDIWGQGTMVT 137

Qy     121 VSS 123
           |||
Db     138 VSS 140


RESULT   7
Q9GYZ2
ID   Q9GYZ2      PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER      1      1
FT   NON_TER    119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;

  Query Match             65.3%;  Score 428;  DB 5;  Length 119;
  Best Local Similarity   66.7%;  Pred. No. 5e-38;
  Matches   82;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||:|||||:|||||||:|||||||:      |::|||||| |||:| |:|: ||| |
Db       1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: |||:| | | |||||:| |||| |:|||||||  || ::  | :|||||||| ||
Db      61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--YYDDH--YCLDYWGQGTTVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT   8
Q9UL95
ID   Q9UL95      PRELIMINARY;      PRT;   125 AA.
AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035019; AAD56255.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C232488EAC CRC64;

  Query Match             65.3%;  Score 428;  DB 4;  Length 125;
  Best Local Similarity   68.8%;  Pred. No. 5.3e-38;
  Matches   86;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||||:|||||||||||||||||||:     |:|||||||| ||||| |:| :| | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
           | |||||:| ||: |||||||| |||:|||||||||    |       | | |||||:
Db      61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120

Qy     119 VTVSS 123
           |||||
Db     121 VTVSS 125


RESULT   9
Q924Q3
ID   Q924Q3       PRELIMINARY;       PRT;   146 AA.
AC   Q924Q3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067797; BAB63282.1; -.
FT   NON_TER       1      1
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16136 MW;  CEA8DD6E1955807F CRC64;

  Query Match             65.2%;  Score 427;  DB 11;  Length 146;
  Best Local Similarity   65.9%;  Pred. No. 8.3e-38;
  Matches   81;  Conservative   17;  Mismatches   23;  Indels    2;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:|||| :| |||
Db       1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :|||||:|||| |||:|||||||  |  :|| ||||||||||| ||
Db      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSLY--DYGDYAMDYWGQGTSVT 118

Qy     121 VSS 123
           |||
Db     119 VSS 121


RESULT  10
Q9D8L4
ID   Q9D8L4       PRELIMINARY;       PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009RIK PROTEIN.
GN   IGH-1 OR 1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

  Query Match             64.4%;  Score 422;  DB 11;  Length 473;
  Best Local Similarity   65.9%;  Pred. No. 1.2e-36;
  Matches   81;  Conservative   19;  Mismatches   19;  Indels    4;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| |||||: |||||||:||||||:    | ||:||:| ||| |||:|:| | :| | |
Db      20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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          : ||:|: |:||| |:|||||:|||| |||:|||:|||| ||  :|  :|  |||||||||
Db      80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY--DYDWFA--YWGQGTLVT 135

Qy     121 VSS 123
           |||
Db     136 VSA 138


RESULT  11
Q924R4
ID   Q924R4       PRELIMINARY;      PRT;   145 AA.
AC   Q924R4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067785; BAB63270.1; -.
FT   NON_TER       1       1
FT   NON_TER     145     145
SQ   SEQUENCE   145 AA;  16081 MW;  ECDB1A135E05B8AA CRC64;


  Query Match             63.4%;  Score 415.5;  DB 11;  Length 145;
  Best Local Similarity   65.0%;  Pred. No. 1.4e-36;
  Matches   80;  Conservative   17;  Mismatches   23;  Indels    3;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:||||| :| |||
Db       1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :||||||:|||| |||:|||||||  |  :|  |||||||||| ||
Db      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDY--DYD-YAMDYWGQGTSVT 117

Qy     121 VSS 123
           |||
Db     118 VSS 120


RESULT  12
Q924R1
ID   Q924R1       PRELIMINARY;      PRT;   145 AA.
AC   Q924R1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067789; BAB63274.1; -.
FT   NON_TER       1       1
FT   NON_TER     145     145
SQ   SEQUENCE   145 AA;  15979 MW;  0162D0A26C746C04 CRC64;


  Query Match             63.4%;  Score 415.5;  DB 11;  Length 145;
  Best Local Similarity   64.2%;  Pred. No. 1.4e-36;
  Matches   79;  Conservative   16;  Mismatches   25;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:||||| :| |||
Db       1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :||||||:|||| |||:|||||||  |     ||||||||| ||
Db      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR---YDGSSFYAMDYWGQGTSVT 117

Qy     121 VSS 123
           |||
Db     118 VSS 120


RESULT  13
Q924R8
ID   Q924R8       PRELIMINARY;      PRT;   146 AA.
AC   Q924R8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067781; BAB63266.1; -.
FT   NON_TER       1       1
FT   NON_TER     146     146
SQ   SEQUENCE   146 AA;  16216 MW;  92460F1FDF1B7538 CRC64;


  Query Match             62.9%;  Score 412;  DB 11;  Length 146;
  Best Local Similarity   63.4%;  Pred. No. 3.3e-36;
  Matches   78;  Conservative   19;  Mismatches   24;  Indels    2;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:||||| :| |||
Db       1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :||||||:|||| |||:|||||||  |||:  :|  ||||||| :|
Db      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR-SYYGS-SLYYFDYWGQGTTLT 118

Qy     121 VSS 123
           |||
Db     119 VSS 121


RESULT  14
Q9UL89
ID   Q9UL89       PRELIMINARY;      PRT;   116 AA.
AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035025; AAD56261.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;


  Query Match             62.8%;  Score 411.5;  DB 4;  Length 116;
  Best Local Similarity   72.5%;  Pred. No. 2.8e-36;
  Matches   87;  Conservative    3;  Mismatches   25;  Indels    5;  Gaps    2;

Qy       5 VQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKF 64
           ||||||||||:|||||||||||       | |||||||| ||||||| |  |   |  ||
Db       1 VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF 60

Qy      65 QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS 123
           ||||||||| | ||||||||||||||||||||||       |:| |   | ||:||||||||
Db      61 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCAS----SNWGPYWYFDLWGRGTLVTVSS 116


RESULT  15
Q924Q6
ID   Q924Q6      PRELIMINARY;      PRT;   145 AA.
AC   Q924Q6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067794; BAB63279.1; -.
FT   NON_TER       1      1
FT   NON_TER     145    145
SQ   SEQUENCE   145 AA;  16011 MW;  9BC0846D40DF97EA CRC64;


  Query Match             62.5%;  Score 409.5;  DB 11;  Length 145;
  Best Local Similarity   63.2%;  Pred. No. 6e-36;
  Matches   79;  Conservative   17;  Mismatches   22;  Indels    7;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:||||| :| |||
Db       1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE--GYYGNYGVYAMDYWGQGTL 118
           : ||: : |:| |  :|||||:|||| |||:||||||    :|     ||||||||||
Db      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSTLSHY-----YAMDYWGQGTS 115

Qy     119 VTVSS 123
           |||||
Db     116 VTVSS 120


Search completed: July  9, 2002, 15:45:36
Job time: 387 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:40:36 ; Search time 51.18 Seconds
(without alignments)
266.942 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	16	AAR81323	Humanized VLA-4 an
2	655	100.0	142	16	AAR81333	Human VLA-4 reshap
3	655	100.0	142	18	AAW22428	Humanised alpha-4
4	648	98.9	123	18	AAW22413	Humanised alpha-4
5	552	84.3	123	16	AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16	AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18	AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19	AAW44124	Heavy chain variab
9	523.5	79.9	431	22	AAB30693	A fusion of single
10	523	79.8	136	16	AAR76681	Human/murine chime
11	523	79.8	136	17	AAW04396	Chimaeric human/mu
12	523	79.8	269	16	AAR76682	Human ONS-M21 anti
13	523	79.8	269	17	AAW04397	Chimaeric human/mu
14	515	78.6	119	16	AAR81325	Humanized VLA-4 an
15	515	78.6	119	18	AAW22426	Humanised alpha-4
16	512	78.2	119	16	AAR81324	Humanized VLA-4 an
17	512	78.2	119	18	AAW22425	Humanised alpha-4
18	507.5	77.5	135	21	AAB07969	A heavy chain vari
19	504.5	77.0	118	14	AAR37611	hIL2R Ab H chain V
20	503	76.8	119	20	AAY52717	Humanised ATR-5 H
21	503	76.8	119	22	AAB74978	Humanised ATR-5 H
22	499	76.2	119	20	AAY52719	Humanised ATR-5 H
23	499	76.2	119	22	AAB74980	Humanised ATR-5 H
24	496	75.7	136	17	AAR92084	Humanised antibody
25	495	75.6	119	16	AAR81331	Human 2*CL antibod
26	493	75.3	119	20	AAY52718	Humanised ATR-5 H
27	493	75.3	119	22	AAB74979	Humanised ATR-5 H
28	492	75.1	117	15	AAR57476	CDR-grafted anti-R
29	492	75.1	117	17	AAR92079	Murine 1308F VH CD
30	492	75.1	136	15	AAR57481	Humanized 1308F VH
31	491	75.0	119	20	AAY52708	Humanised ATR-5 H
32	491	75.0	119	22	AAB74969	Humanised ATR-5 H
33	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
34	489	74.7	119	20	AAY52720	Humanised ATR-5 H
35	489	74.7	119	22	AAB74981	Humanised ATR-5 H
36	487.5	74.4	120	15	AAR47491	Humanised anti-CDI
37	487	74.4	119	20	AAY52712	Humanised ATR-5 H
38	487	74.4	119	20	AAY52715	Humanised ATR-5 H
39	487	74.4	119	22	AAB74973	Humanised ATR-5 H
40	487	74.4	119	22	AAB74976	Humanised ATR-5 H
41	486	74.2	140	18	AAW21847	Humanised heavy ch
42	486	74.2	143	15	AAR59942	Anti-VLA4 rAb huma
43	484.5	74.0	139	14	AAR33953	gH1 variable domai
44	484.5	74.0	139	18	AAW29753	CDR-grafted humani
45	484.5	74.0	139	21	AAY56877	gH1 variable domai

ALIGNMENTS

RESULT 1
AAR81323
ID AAR81323 standard; Protein; 123 AA.
XX
AC AAR81323;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Claim 11; Page 69; 105pp; English.

```
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;

  Query Match             100.0%;  Score 655;  DB 16;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 120

Qy     121 VSS 123
           |||
Db     121 vss 123


RESULT   2
AAR81333
ID   AAR81333 standard; Protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..142
FT                   /note= "framework region 4"
XX

PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions.  In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis.  They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis.  The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   142 AA;

  Query Match             100.0%;  Score 655;  DB 16;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139

Qy     121 VSS 123
           |||
Db     140 vss 142


RESULT   3
AAW22428
ID   AAW22428 standard; Protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
```

```
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Leader
FT   Protein         20..142
FT                   /label= Mat_protein
FT                   /note= "VH version Ha (Claim 25)"
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Region          50..55
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..67
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          68..85
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Region          118..131
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          132..142
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;    96WO-US18807.
XX
PR   21-NOV-1995;    95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413).  It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   142 AA;

  Query Match             100.0%;  Score 655;  DB 18;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139

Qy     121 VSS 123
           |||
Db     140 vss 142


RESULT   4
AAW22413
ID   AAW22413 standard; Protein; 123 AA.
XX
AC   AAW22413;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                         those of MAb 21.6, involved in antigen
FT                         binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                         21.6 VL, important in supporting the CDR2
FT                         loop"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
```

XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 25; Fig 7; 107pp; English.
XX
CC This polypeptide, designated Ha, comprises the heavy chain variable
CC region (VH) of a humanised alpha-4 integrin antibody 21.6. It is
CC composed of complementarity determining regions (CDRs) from the VH
CC region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC 21.6 and a modified human 21/28'CL framework. It can be expressed
CC in mammalian host cells following PCR amplification and mutagenesis
CC of appropriate fragments of mouse and human DNA sequences. The
CC humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC to produce a claimed humanised 21.6 antibody that is useful in the
CC manufacture of a medicament for treating asthma, atherosclerosis,
CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibody has a
CC half-life in the human circulation essentially equivalent to that
CC of naturally occurring human antibodies.
XX
SQ Sequence 123 AA;

Query Match 98.9%; Score 648; DB 18; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.4e-52;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyandywgqgtlvt 120

Qy     121 VSS 123
           |||
Db     121 vss 123
```

RESULT 5
AAR81330
ID AAR81330 standard; Protein; 123 AA.
XX
AC AAR81330;
XX
DT 02-APR-1996 (first entry)
XX
DE Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX

FH Key Location/Qualifiers
FT Region 1..30
FT /label= FR1
FT /note= "mouse heavy chain variable framework
FT region 1"
FT Region 31..35
FT /label= CDR1
FT /note= "mouse heavy chain variable complementarity
FT determining region 1"
FT Region 36..49
FT /label= FR2
FT /note= "mouse heavy chain variable framework
FT region 2"
FT Region 50..66
FT /label= CDR2
FT /note= "mouse heavy chain variable complementarity
FT determining region 2"
FT Region 67..98
FT /label= FR3
FT /note= "mouse heavy chain variable framework
FT region 3"
FT Region 99..112
FT /label= CDR3
FT /note= "mouse heavy chain variable complementarity
FT determining region 3"
FT Region 113..123
FT /label= FR4
FT /note= "mouse heavy light chain variable framework
FT region 4"
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Page 68; 105pp; English.
XX
CC The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC variable region (without signal sequence). Cloned cDNA CDR sequences of
CC mouse 21.6 variable light and variable heavy regions are linked to human
CC constant framework regions of the REI antibody for the light chain and
CC the 2*CL antibody for the heavy chain in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC modified using PCR primers (See AAQ99895-98) and then subcloned into
CC mammalian cell expression vectors containing human kappa or gamma-1
CC constant regions. In the humanized light chain, amino acids L45, L49,
CC L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC acid present in the equivalent position of the mouse 21.6 Ig light
CC chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC cells. The humanized antibodies can be used to inhibit adhesion of a
CC leukocyte to an endothelial cell and to treat inflammatory diseases such
CC as multiple sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC used for detecting VLA-4, for affinity purification or for generating
CC anti-idiotype antibodies.
XX
SQ Sequence 123 AA;

Query Match 84.3%; Score 552; DB 16; Length 123;

```
  Best Local Similarity   82.9%;  Pred. No. 1.7e-43;
  Matches  102;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||| |:| | | |||:||||||||||||
Db       1 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||: |||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      61 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 120

Qy     121 VSS 123
           |||
Db     121 vss 123


RESULT   6
AAR81327
ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-01186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   140 AA;


  Query Match           83.1%;  Score 544;  DB 16;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-42;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||| |:| | | |||:||||||||||||
Db      20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||: |||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139

Qy     121 V 121
           |
Db     140 v 140


RESULT   7
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Leader
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "framework region 3"
```

```
FT   Region          118..131
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;    96WO-US18807.
XX
PR   21-NOV-1995;    95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   140 AA;
```

```
  Query Match             83.1%;  Score 544;  DB 18;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-42;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: ||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db      20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| |||||||:::|||::|||| |||||||:|||||||||||||||||||||| ||
Db      80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139

Qy     121 V 121
           |
Db     140 v 140


RESULT   8
AAW44124
ID   AAW44124 standard; Protein; 120 AA.
XX
AC   AAW44124;
XX
DT   05-JUN-1998  (first entry)
XX
DE   Heavy chain variable region of humanised NR-LU-13 antibody NRX451.
```

```
XX
KW   Heavy chain; variable region; murine; mouse; human; cancer antigen;
KW   antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
KW   treatment.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /note= "complementarity determining region 1"
FT   Region          50..59
FT                   /note= "complementarity determining region 2"
FT   Region          99..109
FT                   /note= "complementarity determining region 3"
FT
XX
PN   WO9746589-A2.
XX
PD   11-DEC-1997.
XX
PF   06-JUN-1997;    97WO-US10074.
XX
PR   07-JUN-1996;    96US-0660362.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Graves SS, Henry AH, Hylarides MD, Mallet RW, Pedersen JT;
PI   Rees AR, Renojm, Searle SMJ;
XX
DR   WPI; 1998-042124/04.
XX
PT   Humanised antibody binds same human cancer antigen as antibody
PT   NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT   therapy and immunodiagnosis
XX
PS   Example 1; Fig 4; 100pp; English.
XX
CC   The present sequence is the heavy chain variable region of the
CC   humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
CC   NRX451.
CC   A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC   hAb, specifically NRX451, or its conjugates can be used for the
CC   manufacture of a diagnostic or medicament for cancer diagnosis or
CC   treatment. The hAb has reduced immunogenicity and toxicity in
CC   humans, but retains the ability to bind the NR-LU-13 antigen.
XX
SQ   Sequence   120 AA;
```

```
  Query Match             79.9%;  Score 523.5;  DB 19;  Length 120;
  Best Local Similarity   82.9%;  Pred. No. 6.9e-41;
  Matches  102;  Conservative    8;  Mismatches   10;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||:||||||| |:|||||||| ||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntkc 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |  |||||||||||| :|||||||||||:|||||||:||      | :::|||||||||
Db      61 disfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117

Qy     121 VSS 123
           |||
Db     118 vss 120


RESULT   9
AAB30693
ID   AAB30693 standard; Protein; 431 AA.
XX
AC   AAB30693;
XX
DT   02-APR-2001  (first entry)
```

```
XX
DE   A fusion of single chain antibody/streptavidin.
XX
KW   Streptavidin; tumour cell; cancer; adenocarcinoma;
KW   hematological malignancy; huNR-LU-10; EGP40; EPCAM.
XX
OS   Synthetic.
OS   Streptomyces avidinii.
OS   Homo sapiens.
XX
PN   WO200075333-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US15595.
XX
PR   07-JUN-1999;   99US-0137900.
PR   03-DEC-1999;   99US-0168976.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Goshorn SC,  Graves SS,  Schultz JE,  Lin Y,  Sanderson JA,  Reno JM;
XX
DR   WPI; 2001-091213/10.
DR   N-PSDB; AAC86562.
XX
PT   New vector constructs for expressing genomic streptavidin fusion
PT   proteins which are useful for targeting tumour cells associated with
PT   cancer, e.g. adenocarcinomas -
XX
PS   Example 1; Fig 10; 100pp; English.
XX
CC   The present sequence encodes a fusion of the single chain antibody
CC   huNR-LU-10 and streptavidin. The antibody binds the antigen EGP40 or
CC   EPCAM. The fusion protein is expressed using vectors of the invention.
CC   The specification describes vector constructs for expressing streptavidin
CC   fusion proteins. The vector comprises a first nucleic acid encoding
CC   streptavidin or its functional variant operatively linked to a promoter,
CC   and a cloning site for insertion of a second nucleic acid sequence
CC   encoding a polypeptide to be fused with streptavidin, interposed between
CC   the promoter and the first nucleic acid sequence. Alternatively, the
CC   vector construct comprises a first nucleic acid, operatively linked to a
CC   promoter, encoding a polypeptide to be fused with streptavidin, and a
CC   cloning site for insertion of a second nucleic acid encoding at least
CC   129 amino acids of streptavidin or its functional variant. The fusion
CC   proteins are useful for targeting tumour cells, particularly tumour cells
CC   associated with cancer, e.g. adenocarcinomas or hematological
CC   malignancies. The vector construct is useful for expressing of
CC   streptavidin fusion proteins. In particular, these are useful as tools
CC   for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC   presence or absence of, or treating, a target site within a mammalian
CC   host.
XX
SQ   Sequence   431 AA;
```

```
  Query Match           79.9%;  Score 523.5;  DB 22;  Length 431;
  Best Local Similarity   82.9%;  Pred. No. 2.8e-40;
  Matches  102;  Conservative    8;  Mismatches   10;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||:|||||||| |:|||||||| ||
Db     148 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntks 207

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |  |||||||||||| :|||||||||||:|||||||:||      | :::||||||||||
Db     208 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 264

Qy     121 VSS 123
           |||
Db     265 vss 267
```

```
RESULT  10
AAR76681
ID   AAR76681 standard; Protein; 136 AA.
XX
AC   AAR76681;
XX
DT   17-JAN-1996  (first entry)
XX
DE   Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
XX
KW   Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..19
FT                    /label= sig_peptide
FT   Peptide          20..50
FT                    /label= FR 1
FT   Peptide          51..55
FT                    /label= CDR 1
FT   Peptide          56..59
FT                    /label= FR 2
FT   Peptide          70..86
FT                    /label= CDR 2
FT   Peptide          87..118
FT                    /label= FR 3
FT   Peptide          119..126
FT                    /label= CDR 3
FT   Peptide          127..136
FT                    /label= FR 4
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94539.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 26; Page 94; 120pp; Japanese.
XX
CC   AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-
CC   RVL-M21g(gamma)1. The antibody is reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   136 AA;
```

```
  Query Match           79.8%;  Score 523;  DB 16;  Length 136;
  Best Local Similarity   83.7%;  Pred. No. 8.8e-41;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||:|||||||||||||||||||||||||||| ||||||||||:| |||
Db      20 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||| | :|||||||||||||| |:||   || |      ||||||| ||
Db      80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133
```

```
Qy     121 VSS 123
           |||
Db     134 vss 136


RESULT  11
AAW04396
ID   AAW04396 standard; Protein; 136 AA.
XX
AC   AAW04396;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..136
FT                   /label= mat_peptide
FT   Region          50..54
FT                   /label= CDR_1
FT   Region          69..85
FT                   /label= CDR_2
FT   Region          118..125
FT                   /label= CDR_3
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38653.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 5; Pages 38-39; 45pp; Japanese.
XX
CC   The present sequence is a fragment of the chimaeric human/murine
CC   monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by
CC   combining light and heavy variable region DNA, from a murine
CC   anti-human myeloblastoma cell MAb, with human light and heavy
CC   constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

 Query Match             79.8%;  Score 523;  DB 17;  Length 136;
  Best Local Similarity   83.7%;  Pred. No. 8.8e-41;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||||| ||||||||||:| |||
Db      20 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db      80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133

Qy     121 VSS 123
           |||
Db     134 vss 136


RESULT  12
AAR76682
ID   AAR76682 standard; Protein; 269 AA.
XX
AC   AAR76682;
XX
DT   18-JAN-1996  (first entry)
XX
DE   Human ONS-M21 antibody Fv fragment.
XX
KW   Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= sig_peptide
FT   Region          23..139
FT                   /note= "heavy variable region"
FT   Region          140..154
FT                   /note= "linker"
FT   Region          155..269
FT                   /note= "light variable region"
FT   Region          262..269
FT                   /note= "FLAG"
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94548.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 35; Pages 98-99; 120pp; Japanese.
XX
CC   AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the
CC   human antibody ONS-M21 Fv fragment. The plasmid was used in the
CC   construction of an expression vector, contg. cDNA encoding a
CC   human/murine chimeric antibody, reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   269 AA;
```

```
  Query Match             79.8%;  Score 523;  DB 16;  Length 269;
  Best Local Similarity   83.7%;  Pred. No. 1.9e-40;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||||| |||||||||:| |||
Db      23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||| | :|||||||||||||||| |:||   || |       ||||||| ||
Db      83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136

Qy     121 VSS 123
           |||
Db     137 vss 139


RESULT  13
AAW04397
ID   AAW04397 standard; Protein; 269 AA.
XX
AC   AAW04397;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 scFv fragment.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= sig_peptide
FT   Region          23..139
FT                   /note= "heavy variable region"
FT   Peptide         140..154
FT                   /label= linker
FT   Region          155..261
FT                   /note= "light variable region"
FT   Peptide         262..269
FT                   /label= FLAG
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38662.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 6; Pages 40-41; 45pp; Japanese.
XX
CC   The present sequence is a scFv fragment from the chimaeric
CC   human/murine monoclonal antibody (MAb) ONS-M21. The MAb was
CC   prepd. by combining light and heavy variable region DNA, from a
CC   murine anti-human myeloblastoma cell MAb, with human light and
CC   heavy constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   269 AA;


  Query Match             79.8%;  Score 523;  DB 17;  Length 269;
  Best Local Similarity   83.7%;  Pred. No. 1.9e-40;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||||| |||||||||:| |||
Db      23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||| | :|||||||||||||||| |:||   || |       ||||||| ||
Db      83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136

Qy     121 VSS 123
           |||
Db     137 vss 139


RESULT  14
AAR81325
ID   AAR81325 standard; Protein; 119 AA.
XX
AC   AAR81325;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 13; Page 70; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
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```
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   119 AA;

  Query Match             78.6%;  Score 515;  DB 16;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 4.1e-40;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||  :|||||||||||||| |:  || |||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfnlksyamhwvrqapgqrlewmgwinagngntky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||| ||:|:     :|||||||||
Db      61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116

Qy     121 VSS 123
           |||
Db     117 vss 119


RESULT  15
AAW22426
ID   AAW22426 standard; Protein; 119 AA.
XX
AC   AAW22426;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Hc.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                          those of MAb 21.6, involved in antigen
FT                          binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                          21.6 VL, important in supporting the CDR2
FT                          loop"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Misc-difference 102
FT                   /note= "21/28'CL Tyr-102 is substd. by Phe of human
FT                          VCAM-1"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 5; Fig 7; 107pp; English.
XX
CC   This polypeptide, designated Hc, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6.  It is
CC   composed of complementarity determining regions (CDRs) from the VH
CC   region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human 21/28'CL framework.  It contains an
CC   additional amino acid substitution (Tyr102Phe) in comparison to
CC   claimed humanised 21.6 VH version Ha (see AAW22412).  Humanised
CC   21.6 VH and VL regions are used to produce claimed humanised 21.6
CC   antibodies useful in the manufacture of a medicament for treating
CC   asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC   bowel disease, rheumatoid arthritis, transplant rejection, graft
CC   versus host disease, tumour metastasis, nephritis, atopic
CC   dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC   mediated lung injury.  The humanised antibodies have a half-life
CC   in the human circulation essentially equivalent to that of
CC   naturally occurring human antibodies.
XX
SQ   Sequence   119 AA;

  Query Match             78.6%;  Score 515;  DB 18;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 4.1e-40;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||  :|||||||||||||| |:  || |||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||| ||:|:     :|||||||||
Db      61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116

Qy     121 VSS 123
           |||
Db     117 vss 119


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